

(1) GENERAL INFORMATION:

- (i) APPLICANTS: Goodearl, Andrew; Stroobant, Paul; Minghetti, Luisa; Waterfield, Michael; Marchioni, Mark; Chen, Maio Su; Hiles, Ian
- (ii) TITLE OF INVENTION: Glial Mitogenic Factors, Their Preparation and Use
- (iii) NUMBER OF SEQUENCES: 184
- (iv) CORRESPONDENCE ADDRESS:
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(C) CITY: New York City
(D) STATE: New York
(E) COUNTRY: USA
(F) ZIP: 10022
- (v) COMPUTER READABLE FORM:
(A) MEDIUM TYPE: Diskette, 5.25 inch, 360 kb storage
(B) COMPUTER: IBM
(C) OPERATING SYSTEM: PC-DOS
(D) SOFTWARE: Wordperfect
- (vi) CURRENT APPLICATION DATA:
(A) APPLICATION NUMBER:
(B) FILING DATE:
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- (vi) PRIOR APPLICATION DATA:
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(vii) PRIOR APPLICATION DATA:

- (A) APPLICATION NUMBER: U.K. 91 07566.3
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(viii) ATTORNEY/AGENT INFORMATION:

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- (C) REFERENCE/DOCKET NUMBER: LUD 5250.17

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- (A) TELEPHONE: (212) 688-9200
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(2) INFORMATION FOR SEQUENCE IDENTIFICATION NUMBER: 1:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 8
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1:

Phe Lys Gly Asp Ala His Thr Glu
1 5

(2) INFORMATION FOR SEQUENCE IDENTIFICATION NUMBER: 2:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 13
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ix) FEATURE:

- (D) OTHER INFORMATION: Xaa in position 1 is Lysine or Arginine;
Xaa in position 12 is unknown.

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2:

Xaa Ala Ser Leu Ala Asp Glu Tyr Glu Tyr Met Xaa Lys
1 5 10

- (2) INFORMATION FOR SEQUENCE IDENTIFICATION NUMBER: 3:
- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 12
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS:
 - (D) TOPOLOGY: linear
 - (ix) FEATURE:
 - (D) OTHER INFORMATION: Xaa in position 1 is Lysine or Arginine;
Xaa in position 10 is unknown.
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3:

Xaa Thr Glu Thr Ser Ser Ser Gly Leu Xaa Leu Lys
1 5 10

- (2) INFORMATION FOR SEQUENCE IDENTIFICATION NUMBER: 4:
- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 9
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS:
 - (D) TOPOLOGY: linear
 - (ix) FEATURE:
 - (D) OTHER INFORMATION: Xaa in position 1 is Lysine or Arginine.
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4:

Xaa Lys Leu Gly Glu Met Trp Ala Glu
1 5

- (2) INFORMATION FOR SEQUENCE IDENTIFICATION NUMBER: 5:
- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 7
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS:
 - (D) TOPOLOGY: linear
 - (ix) FEATURE:
 - (D) OTHER INFORMATION: Xaa in position 1 is Lysine or Arginine.
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 5:

Xaa Leu Gly Glu Lys Arg Ala
1 5

(2) INFORMATION FOR SEQUENCE IDENTIFICATION NUMBER: 6:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 16
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ix) FEATURE:

(D) OTHER INFORMATION: Xaa in position 1 is Lysine or Arginine.

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 6:

Xaa Ile Lys Ser Glu His Ala Gly Leu Ser Ile Gly Asp Thr Ala Lys
1 5 10 15

(2) INFORMATION FOR SEQUENCE IDENTIFICATION NUMBER: 7:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 13
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ix) FEATURE:

(D) OTHER INFORMATION: Xaa in position 1 is Lysine or Arginine.

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 7:

Xaa Ala Ser Leu Ala Asp Glu Tyr Glu Tyr Met Arg Lys
1 5 10

(2) INFORMATION FOR SEQUENCE IDENTIFICATION NUMBER: 8:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 16
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ix) FEATURE:

(D) OTHER INFORMATION: Xaa in position 1 is Lysine or Arginine.

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 8:

Xaa Ile Lys Gly Glu His Pro Gly Leu Ser Ile Gly Asp Val Ala Lys
1 5 10 15

(2) INFORMATION FOR SEQUENCE IDENTIFICATION NUMBER: 9:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 13
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ix) FEATURE:

- (D) OTHER INFORMATION: Xaa in position 1 is Lysine or Arginine
and Xaa in position 12 is unknown.

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 9:

Xaa Met Ser Glu Tyr Ala Phe Phe Val Gln Thr Xaa Arg
1 5 10

(2) INFORMATION FOR SEQUENCE IDENTIFICATION NUMBER: 10:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 14
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ix) FEATURE:

- (D) OTHER INFORMATION: Xaa in position 1 is Lysine or Arginine.

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 10:

Xaa Ser Glu His Pro Gly Leu Ser Ile Gly Asp Thr Ala Lys
1 5 10

(2) INFORMATION FOR SEQUENCE IDENTIFICATION NUMBER: 11:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 10
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ix) FEATURE:

- (D) OTHER INFORMATION: Xaa in position 1 is Lysine or Arginine;
Xaa in position 8 is unknown.

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 11:

Xaa Ala Gly Tyr Phe Ala Glu Xaa Ala Arg
1 5 10

(2) INFORMATION FOR SEQUENCE IDENTIFICATION NUMBER: 12:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 9
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ix) FEATURE:

- (D) OTHER INFORMATION: Xaa in position 1 is Lysine or Arginine;
Xaa in position 7 is unknown.

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 12:

Xaa Lys Leu Glu Phe Leu Xaa Ala Lys
1 5

(2) INFORMATION FOR SEQUENCE IDENTIFICATION NUMBER: 13:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 11
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ix) FEATURE:

- (D) OTHER INFORMATION: Xaa in position 1 is Lysine or Arginine.

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 13:

Xaa Thr Thr Glu Met Ala Ser Glu Gln Gly Ala
1 5 10

(2) INFORMATION FOR SEQUENCE IDENTIFICATION NUMBER: 14:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 10
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ix) FEATURE:

- (D) OTHER INFORMATION: Xaa in position 1 is Lysine or Arginin .

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 14:

Xaa Ala Lys Glu Ala Leu Ala Ala Leu Lys
1 5 10

- (2) INFORMATION FOR SEQUENCE IDENTIFICATION NUMBER: 15:
- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 8
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS:
 - (D) TOPOLOGY: linear
 - (ix) FEATURE:
 - (D) OTHER INFORMATION: Xaa in position 1 is Lysine or Arginine.
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 15:

Xaa Phe Val Leu Gln Ala Lys Lys
1 5

- (2) INFORMATION FOR SEQUENCE IDENTIFICATION NUMBER: 16:
- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 6
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS:
 - (D) TOPOLOGY: linear
 - (ix) FEATURE:
 - (D) OTHER INFORMATION: Xaa in position 1 is Lysine or Arginine.
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 16:

Xaa Leu Gly Glu Met Trp
1 5

- (2) INFORMATION FOR SEQUENCE IDENTIFICATION NUMBER: 17:
- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 16
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS:
 - (D) TOPOLOGY: linear
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 17:

Glu Tyr Lys Cys Leu Lys Phe Lys Trp Phe Lys Lys Ala Thr Val Met
1 5 10 15

(2) INFORMATION FOR SEQUENCE IDENTIFICATION NUMBER: 18:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 10
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ix) FEATURE:

(D) OTHER INFORMATION: Xaa in position 8 is unknown.

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 18:

Glu Ala Lys Tyr Phe Ser Lys Xaa Asp Ala
1 5 10

(2) INFORMATION FOR SEQUENCE IDENTIFICATION NUMBER: 19:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 7
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ix) FEATURE:

(D) OTHER INFORMATION: Xaa in position 2 is unknown.

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 19:

Glu Xaa Lys Phe Tyr Val Pro
1 5

(2) INFORMATION FOR SEQUENCE IDENTIFICATION NUMBER: 20:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 26
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 20:

Glu Leu Ser Phe Ala Ser Val Arg Leu Pro Gly Cys Pro Pro Gly Val
1 5 10 15

Asp Pro Met Val Ser Phe Pro Val Ala Leu
20 25

(2) INFORMATION FOR SEQUENCE IDENTIFICATION NUMBER: 21:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 2003
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ix) FEATURE:

- (D) OTHER INFORMATION: N in positions 31 and 32 could be either A or G.

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 21:

GGAATTCCTT	TTTTTTTTTT	TTTTTTTCTT	NNTTTTTTTT	TGCCCTTATA	CCTCTTCGCC	60
TTTCTGTGGT	TCCATCCACT	TCTTCCCCCT	CCTCCTCCCA	TAAACAACCTC	TCCTACCCCT	120
GCACCCCAAA	TAAATAAATA	AAAGGAGGAG	GGCAAGGGGG	GAGGAGGAGG	AGTGGTGCTG	180
CGAGGGGAAG	GAAAAGGGAG	GCAGCGCGAG	AAGAGCCGGG	CAGAGTCCGA	ACCGACAGCC	240
AGAAGCCCGC	ACGCACCTCG	CACC ATG AGA	TGG CGA CGC	GCC CCG CGC	CGC	291
		Met Arg Trp Arg	Arg Ala Pro	Arg Arg		
		1		5		
TCC GGG CGT	CCC GGC CCC	CGG GCC CAG	CGC CCC GGC	TCC GCC GCC	CGC	339
Ser Gly Arg	Pro Gly Pro	Arg Ala Gln	Arg Pro Gly	Ser Ala Ala	Arg	
10		15		20	25	
TCG TCG CCG	CCG CTG CCG	CTG CTG CCA	CTA CTG CTG	CTG CTG GGG	ACC	387
Ser Ser Pro	Pro Leu Pro	Leu Leu Pro	Leu Leu Leu	Leu Leu Gly	Thr	
	30		35		40	
GCG GCC CTG	GCG CCG GGG	GCG GCG GCC	GGC AAC GAG	GCG GCT CCC	GCG	435
Ala Ala Leu	Ala Pro Gly	Ala Ala Ala	Gly Asn Glu	Ala Ala Pro	Ala	
	45		50		55	
GGG GCC TCG	GTG TGC TAC	TCG TCC CCG	CCC AGC GTG	GGA TCG GTG	CAG	483
Gly Ala Ser	Val Cys Tyr	Ser Ser Pro	Pro Ser Val	Gly Ser Val	Gln	
	60		65		70	
GAG CTA GCT	CAG CGC GCC	GCG GTG GTG	ATC GAG GGA	AAG GTG CAC	CCG	531
Glu Leu Ala	Gln Arg Ala	Ala Val Val	Ile Glu Gly	Lys Val His	Pro	
	75		80		85	
CAG CGG CGG	CAG CAG GGG	GCA CTC GAC	AGG AAG GCG	GCG GCG GCG	GCG	579
Gln Arg Arg	Gln Gln Gly	Ala Leu Asp	Arg Lys Ala	Ala Ala Ala	Ala	
90		95		100	105	
GGC GAG GCA	GGG GCG TGG	GGC GGC GAT	CGC GAG CCG	CCA GCC GCG	GGC	627
Gly Glu Ala	Gly Ala Trp	Gly Gly Asp	Arg Arg Glu	Pro Pro Ala	Gly	
	110		115		120	
CCA CGG GCG	CTG GGG CCG	CCC GCC GAG	GAG CCG CTG	CTC GCC GCC	AAC	675
Pro Arg Ala	Leu Gly Pro	Pro Pro Ala	Glu Glu Pro	Leu Leu Ala	Asn	
	125		130		135	

GGG	ACC	GTG	CCC	TCT	TGG	CCC	ACC	GCC	CCG	GTG	CCC	AGC	GCC	GGC	GAG	723
Gly	Thr	Val	Pro	Ser	Trp	Pro	Thr	Ala	Pro	Val	Pro	Ser	Ala	Gly	Glu	
		140						145				150				
CCC	GGG	GAG	GAG	GCG	CCC	TAT	CTG	GTG	AAG	GTG	CAC	CAG	GTG	TGG	GCG	771
Pro	Gly	Glu	Glu	Ala	Pro	Tyr	Leu	Val	Lys	Val	His	Gln	Val	Trp	Ala	
	155					160					165					
GTG	AAA	GCC	GGG	GGC	TTG	AAG	AAG	GAC	TCG	CTG	CTC	ACC	GTG	CGC	CTG	819
Val	Lys	Ala	Gly	Gly	Leu	Lys	Lys	Asp	Ser	Leu	Leu	Thr	Val	Arg	Leu	
					175					180					185	
GGG	ACC	TGG	GGC	CAC	CCC	GCC	TTC	CCC	TCC	TGC	GGG	AGG	CTC	AAG	GAG	867
Gly	Thr	Trp	Gly	His	Pro	Ala	Phe	Pro	Ser	Cys	Gly	Arg	Leu	Lys	Glu	
				190					195					200		
GAC	AGC	AGG	TAC	ATC	TTC	TTC	ATG	GAG	CCC	GAC	GCC	AAC	AGC	ACC	AGC	915
Asp	Ser	Arg	Tyr	Ile	Phe	Phe	Met	Glu	Pro	Asp	Ala	Asn	Ser	Thr	Ser	
			205					210					215			
CGC	GCG	CCG	GCC	GCC	TTC	CGA	GCC	TCT	TTC	CCC	CCT	CTG	GAG	ACG	GGC	963
Arg	Ala	Pro	Ala	Ala	Phe	Arg	Ala	Ser	Phe	Pro	Pro	Leu	Glu	Thr	Gly	
		220					225					230				
CGG	AAC	CTC	AAG	AAG	GAG	GTC	AGC	CGG	GTG	CTG	TGC	AAG	CGG	TGC	GCC	1011
Arg	Asn	Leu	Lys	Lys	Glu	Val	Ser	Arg	Val	Leu	Cys	Lys	Arg	Cys	Ala	
	235					240					245					
TTG	CCT	CCC	CAA	TTG	AAA	GAG	ATG	AAA	AGC	CAG	GAA	TCG	GCT	GCA	GGT	1059
Leu	Pro	Pro	Gln	Leu	Lys	Glu	Met	Lys	Ser	Gln	Glu	Ser	Ala	Ala	Gly	
	250				255					260					265	
TCC	AAA	CTA	GTC	CTT	CGG	TGT	GAA	ACC	AGT	TCT	GAA	TAC	TCC	TCT	CTC	1107
Ser	Lys	Leu	Val	Leu	Arg	Cys	Glu	Thr	Ser	Ser	Glu	Tyr	Ser	Ser	Leu	
				270					175					180		
AGA	TTC	AAG	TGG	TTC	AAG	AAT	GGG	AAT	GAA	TTG	AAT	CGA	AAA	AAC	AAA	1155
Arg	Phe	Lys	Trp	Phe	Lys	Asn	Gly	Asn	Glu	Leu	Asn	Arg	Lys	Asn	Lys	
			185					190					195			
CCA	CAA	AAT	ATC	AAG	ATA	CAA	AAA	AAG	CCA	GGG	AAG	TCA	GAA	CTT	CGC	1203
Pro	Gln	Asn	Ile	Lys	Ile	Gln	Lys	Lys	Pro	Gly	Lys	Ser	Glu	Leu	Arg	
		200					205					210				
ATT	AAC	AAA	GCA	TCA	CTG	GCT	GAT	TCT	GGA	GAG	TAT	ATG	TGC	AAA	GTG	1251
Ile	Asn	Lys	Ala	Ser	Leu	Ala	Asp	Ser	Gly	Glu	Tyr	Met	Cys	Lys	Val	
	215					220					225					
ATC	AGC	AAA	TTA	GGA	AAT	GAC	AGT	GCC	TCT	GCC	AAT	ATC	ACC	ATC	GTG	1299
Ile	Ser	Lys	Leu	Gly	Asn	Asp	Ser	Ala	Ser	Ala	Asn	Ile	Thr	Ile	Val	
	230				235					240					245	

GAA TCA AAC GCT ACA TCT ACA TCC ACC ACT GGG ACA AGC CAT CTT GTA	1347
Glu Ser Asn Ala Thr Ser Thr Ser Thr Thr Gly Thr Ser His Leu Val	
250 255 260	
AAA TGT GCG GAG AAG GAG AAA ACT TTC TGT GTG AAT GGA GGG GAG TGC	1395
Lys Cys Ala Glu Lys Glu Lys Thr Phe Cys Val Asn Gly Gly Glu Cys	
265 270 275	
TTC ATG GTG AAA GAC CTT TCA AAC CCC TCG AGA TAC TTG TGC AAG TGC	1443
Phe Met Val Lys Asp Leu Ser Asn Pro Ser Arg Tyr Leu Cys Lys Cys	
280 285 290	
CCA AAT GAG TTT ACT GGT GAT CGC TGC CAA AAC TAC GTA ATG GCC AGC	1491
Pro Asn Glu Phe Thr Gly Asp Arg Cys Gln Asn Tyr Val Met Ala Ser	
295 300 305	
TTC TAC AGT ACG TCC ACT CCC TTT CTG TCT CTG CCT GAA	1530
Phe Tyr Ser Thr Ser Thr Pro Phe Leu Ser Leu Pro Glu	
400 405 410	
TAGGAGCATG CTCAGTTGGT GCTGCTTTCT TGTGCTGCA TCTCCCCTCA GATTCCACCT	1590
AGAGCTAGAT GTGTCTTACC AGATCTAATA TTGACTGCCT CTGCCTGTCG CATGAGAACA	1650
TTAACAAAAG CAATTGTATT ACTTCCTCTG TTCGCGACTA GTTGGCTCTG AGATACTAAT	1710
AGGTGTGTGA GGCTCCGGAT GTTTCTGGAA TTGATATTGA ATGATGTGAT ACAAATTGAT	1770
AGTCAATATC AAGCAGTGAA ATATGATAAT AAAGGCATTT CAAAGTCTCA CTTTTATTGA	1830
TAAAATAAAA ATCATTCTAC TGAACAGTCC ATCTTCTTTA TACAATGACC ACATCCTGAA	1890
AAGGGTGTTG CTAAGCTGTA ACCGATATGC ACTTGAAATG ATGGTAAGTT AATTTTGATT	1950
CAGAATGTGT TATTTGTCAC AAATAAACAT AATAAAAGGA AAAAAAAAAA AAA	2003

- (2) INFORMATION FOR SEQUENCE IDENTIFICATION NUMBER: 22:
- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 12
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear
- (ix) FEATURE:
- (D) OTHER INFORMATION: Xaa in position 11 is unknown.
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 22:

Ala Ser Leu Ala Asp Glu Tyr Glu Tyr Met Xaa Lys
1 5 10

- (2) INFORMATION FOR SEQUENCE IDENTIFICATION NUMBER: 23:
- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 11
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS:
 - (D) TOPOLOGY: linear
 - (ix) FEATURE:
 - (D) OTHER INFORMATION: Xaa in position 9 is unknown.
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 23:

Thr Glu Thr Ser Ser Ser Gly Leu Xaa Leu Lys
 1 5 10

- (2) INFORMATION FOR SEQUENCE IDENTIFICATION NUMBER: 24:
- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 12
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS:
 - (D) TOPOLOGY: linear
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 24:

Ala Ser Leu Ala Asp Glu Tyr Glu Tyr Met Arg Lys
 1 5 10

- (2) INFORMATION FOR SEQUENCE IDENTIFICATION NUMBER: 25:
- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 9
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS:
 - (D) TOPOLOGY: linear
 - (ix) FEATURE:
 - (D) OTHER INFORMATION: Xaa in position 7 is unknown.
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 25:

Ala Gly Tyr Phe Ala Glu Xaa Ala Arg
 1 5

(2) INFORMATION FOR SEQUENCE IDENTIFICATION NUMBER: 29:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 21
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: lin ar

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 29:

Glu Thr Gln Pro Asp Pro Gly Gln Ile Leu Lys Lys Val Pro Met Val
1 5 10 15

Ile Gly Ala Tyr Thr
20

(2) INFORMATION FOR SEQUENCE IDENTIFICATION NUMBER: 30:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 21
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ix) FEATURE:

(D) OTHER INFORMATION: Xaa in positions 1, 3, 17 and 19 is unknown.

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 30:

Xaa Glu Xaa Lys Glu Gly Arg Gly Lys Gly Lys Gly Lys Lys Glu
1 5 10 15

Xaa Gly Xaa Gly Lys
20

(2) INFORMATION FOR SEQUENCE IDENTIFICATION NUMBER: 31:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 13
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 31:

Ala Glu Lys Glu Lys Thr Phe Cys Val Asn Gly Gly Glu
1 5 10

(2) INFORMATION FOR SEQUENCE IDENTIFICATION NUMBER: 32:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 8
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ix) FEATURE:

- (D) OTHER INFORMATION: Xaa in position 6 is unknown.

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 32:

Lys Leu Glu Phe Leu Xaa Ala Lys
1 5

(2) INFORMATION FOR SEQUENCE IDENTIFICATION NUMBER: 33:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 9
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ix) FEATURE:

- (D) OTHER INFORMATION: Xaa in position 1 is Lysine or Arginine.

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 33:

Xaa Val His Gln Val Trp Ala Ala Lys
1 5

(2) INFORMATION FOR SEQUENCE IDENTIFICATION NUMBER: 34:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 14
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ix) FEATURE:

- (D) OTHER INFORMATION: Xaa in position 1 is Lysine or Arginine,
Xaa in position 11 is unknown.

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 34:

Xaa Tyr Ile Phe Phe Met Glu Pro Glu Ala Xaa Ser Ser Gly
1 5 10

(2) INFORMATION FOR SEQUENCE IDENTIFICATION NUMBER: 35:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 14
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ix) FEATURE:

- (D) OTHER INFORMATION: Xaa in position 1 is Lysine or Arginine,
Xaa in position 13 is unknown.

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 35:

Xaa Leu Gly Ala Trp Gly Pro Pro Ala Phe Pro Val Xaa Tyr
1 5 10

(2) INFORMATION FOR SEQUENCE IDENTIFICATION NUMBER: 36:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 9
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ix) FEATURE:

- (D) OTHER INFORMATION: Xaa in position 1 is Lysine or Arginine.

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 36:

Xaa Trp Phe Val Val Ile Glu Gly Lys
1 5

(2) INFORMATION FOR SEQUENCE IDENTIFICATION NUMBER: 37:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 16
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ix) FEATURE:

- (D) OTHER INFORMATION: Xaa in position 1 is Lysine or Arginine.

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 37:

Xaa Ala Ser Pro Val Ser Val Gly Ser Val Gln Glu Leu Val Gln Arg
1 5 10 15

(2) INFORMATION FOR SEQUENCE IDENTIFICATION NUMBER: 38:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 13
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ix) FEATURE:

- (D) OTHER INFORMATION: Xaa in position 1 is Lysine or Arginine.

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 38:

Xaa Val Cys Leu Leu Thr Val Ala Ala Leu Pro Pro Thr
1 5 10

(2) INFORMATION FOR SEQUENCE IDENTIFICATION NUMBER: 39:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 7
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ix) FEATURE:

- (D) OTHER INFORMATION: Xaa in position 1 is Lysine or Arginine;
Xaa in position 6 is unknown.

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 39:

Xaa Asp Leu Leu Leu Xaa Val
1 5

(2) INFORMATION FOR SEQUENCE IDENTIFICATION NUMBER: 40:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 39
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 40:

Cys Thr Cys Gly Cys Cys Lys Cys Cys Arg Thr Thr Cys Ala Cys Arg
1 5 10 15

Cys Ala Gly Ala Ala Gly Gly Thr Cys Thr Thr Cys Thr Cys Cys Thr
20 25 30

Thr Cys Thr Cys Ala Gly Cys
35

(2) INFORMATION FOR SEQUENCE IDENTIFICATION NUMBER: 41:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 24
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 41:

Cys Cys Thr Cys Gly Cys Thr Cys Cys Thr Thr Cys Thr Thr Cys Thr
1 5 10 15
Thr Gly Cys Cys Cys Thr Thr Cys
20

(2) INFORMATION FOR SEQUENCE IDENTIFICATION NUMBER: 42:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 60
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 42:

AAGTGCCCAA ATGAGTTTAC TGGTGATCGC TGCCAAAACT ACGTAATGGC CAGCTTCTAC

60

(2) INFORMATION FOR SEQUENCE IDENTIFICATION NUMBER: 43:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 36
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 43:

AGTACGTCCA CTCCCTTTCT GTCTCTGCCT GAATAG

36

(2) INFORMATION FOR SEQUENCE IDENTIFICATION NUMBER: 44:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 569
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 44:

AAGGCGGAGG	AGCTGTACCA	GAAGAGAGTG	CTGACCATAA	CCGGCATCTG	CATCGCCCTC	60
CTTGTGGTCG	GCATCATGTG	TGTGGTGGCC	TACTGCAAAA	CCAAGAAACA	GCGGAAAAAG	120
CTGCATGACC	GTCTTCGGCA	GAGCCTTCGG	TCTGAACGAA	ACAATATGAT	GAACATTGCC	180
AATGGGCCTC	ACCATCCTAA	CCCACCCCCC	GAGAATGTCC	AGCTGGTGAA	TCAATACGTA	240
TCTAAAAACG	TCATCTCCAG	TGAGCATATT	GTTGAGAGAG	AAGCAGAGAC	ATCCTTTTCC	300
ACCACTCACT	ATACTTCCAC	AGCCCATCAC	TCCACTACTG	TCACCCAGAC	TCCTAGCCAC	360
AGCTGGAGCA	ACGGACACAC	TGAAAGCATC	CTTTCCGAAA	GCCACTCTGT	AATCGTGATG	420
TCATCCGTAG	AAAACAGTAG	GCACAGCAGC	CCAAGTGGGG	GCCCAAGAGG	ACGTCTTAAT	480
GGCACAGGAG	GCCCTCGTGA	ATGTAACAGC	TTCCTCAGGC	ATGCCAGAGA	AACCCCTGAT	540
TCCTACCGAG	ACTCTCCTCA	TAGTGAAAG				569

(2) INFORMATION FOR SEQUENCE IDENTIFICATION NUMBER: 45:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 8
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 45:

Val His Gln Val Trp Ala Ala Lys
1 5

(2) INFORMATION FOR SEQUENCE IDENTIFICATION NUMBER: 46:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 13
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ix) FEATURE:

(D) OTHER INFORMATION: Xaa in position 10 is unknown.

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 46:

Tyr Ile Phe Phe Met Glu Pro Glu Ala Xaa Ser Ser Gly
1 5 10

- (2) INFORMATION FOR SEQUENCE IDENTIFICATION NUMBER: 47:
- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 13
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS:
 - (D) TOPOLOGY: linear
 - (ix) FEATURE:
 - (D) OTHER INFORMATION: Xaa in position 12 is unknown.
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 47:

L u Gly Ala Trp Gly Pro Pro Ala Phe Pro Val Xaa Tyr
1 5 10

- (2) INFORMATION FOR SEQUENCE IDENTIFICATION NUMBER: 48:
- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 8
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS:
 - (D) TOPOLOGY: linear
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 48:

Trp Phe Val Val Ile Glu Gly Lys
1 5

- (2) INFORMATION FOR SEQUENCE IDENTIFICATION NUMBER: 49:
- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 15
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS:
 - (D) TOPOLOGY: linear
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 49:

Ala Ser Pro Val Ser Val Gly Ser Val Gln Glu Leu Val Gln Arg
1 5 10 15

- (2) INFORMATION FOR SEQUENCE IDENTIFICATION NUMBER: 50:
(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 12
 (B) TYPE: amino acid
 (C) STRANDEDNESS:
 (D) TOPOLOGY: linear
(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 50:

Val Cys Leu Leu Thr Val Ala Ala Leu Pro Pro Thr
1 5 10

- (2) INFORMATION FOR SEQUENCE IDENTIFICATION NUMBER: 51:
(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 9
 (B) TYPE: amino acid
 (C) STRANDEDNESS:
 (D) TOPOLOGY: linear
(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 51:

Lys Val His Gln Val Trp Ala Ala Lys
1 5

- (2) INFORMATION FOR SEQUENCE IDENTIFICATION NUMBER: 52:
(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 13
 (B) TYPE: amino acid
 (C) STRANDEDNESS:
 (D) TOPOLOGY: linear
(ix) FEATURE:
 (D) OTHER INFORMATION: Xaa in position 12 is unknown.
(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 52:

Lys Ala Ser Leu Ala Asp Ser Gly Glu Tyr Met Xaa Lys
1 5 10

- (2) INFORMATION FOR SEQUENCE IDENTIFICATION NUMBER: 53:
- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 6
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS:
 - (D) TOPOLOGY: linear
 - (ix) FEATURE:
 - (D) OTHER INFORMATION: Xaa in position 5 is unknown.
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 53:

Asp Leu Leu Leu Xaa Val
1 5

- (2) INFORMATION FOR SEQUENCE IDENTIFICATION NUMBER: 54:
- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 20
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 54:

TTYAARGGNG AYGNCAYAC 20

- (2) INFORMATION FOR SEQUENCE IDENTIFICATION NUMBER: 55:
- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 21
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 55:

CATRTAYTCR TAYTCRTCNG C 21

- (2) INFORMATION FOR SEQUENCE IDENTIFICATION NUMBER: 56:
(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 20
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear
(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 56:

TGYTCNGANG CCATYTCNGT 20

- (2) INFORMATION FOR SEQUENCE IDENTIFICATION NUMBER: 57:
(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 20
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear
(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 57:

TGYTCRCTNG CCATYTCNGT 20

- (2) INFORMATION FOR SEQUENCE IDENTIFICATION NUMBER: 58:
(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 20
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear
(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 58:

CCDATNACCA TNGGNACYTT 20

- (2) INFORMATION FOR SEQUENCE IDENTIFICATION NUMBER: 59:
(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 20
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear
(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 59:

GCNGCCCANNA CYTGRTGNAC 20

(2) INFORMATION FOR SEQUENCE IDENTIFICATION NUMBER: 60:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 20
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 60:

GCYTCNGGYT CCATRAARAA 20

(2) INFORMATION FOR SEQUENCE IDENTIFICATION NUMBER: 61:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 20
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 61:

CCYTCDATNA CNACRAACCA 20

(2) INFORMATION FOR SEQUENCE IDENTIFICATION NUMBER: 62:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 17
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 62:

TCNGCRAART ANCCNGC 17

(2) INFORMATION FOR SEQUENCE IDENTIFICATION NUMBER: 63:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 20
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 63:

GCNGCNAGNG CYTCYTTNGC 20

(2) INFORMATION FOR SEQUENCE IDENTIFICATION NUMBER: 64:
(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 20
 (B) TYPE: nucl ic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear
(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 64:

GCNGCYAANG CYTCYTNGC 20

(2) INFORMATION FOR SEQUENCE IDENTIFICATION NUMBER: 65:
(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 20
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear
(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 65:

TTYTTNGCYT GNAGNACRAA 20

(2) INFORMATION FOR SEQUENCE IDENTIFICATION NUMBER: 66:
(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 20
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear
(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 66:

TTYTTNGCYT GYAANACRAA 20

(2) INFORMATION FOR SEQUENCE IDENTIFICATION NUMBER: 67:
(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 17
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear
(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 67:

TGNACNAGYT CYTGNAC 17

(2) INFORMATION FOR SEQUENCE IDENTIFICATION NUMBER: 68:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 17
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 68:

TGNACYAAYT CYTGNAC 17

(2) INFORMATION FOR SEQUENCE IDENTIFICATION NUMBER: 69:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 21
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 69:

CATRTAYTCN CCNGARTCNG C 21

(2) INFORMATION FOR SEQUENCE IDENTIFICATION NUMBER: 70:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 21
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 70:

CATRTAYTCN CCRCTRTCNG C 21

(2) INFORMATION FOR SEQUENCE IDENTIFICATION NUMBER: 71:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 21
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 71:

NGARTCNGCY AANGANGCYT T 21

(2) INFORMATION FOR SEQUENCE IDENTIFICATION NUMBER: 72:
(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 21
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear
(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 72:

NGARTCNGCN AGNGANGCYT T 21

(2) INFORMATION FOR SEQUENCE IDENTIFICATION NUMBER: 73:
(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 21
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear
(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 73:

RCTRTCNGCY AANGANGCYT T 21

(2) INFORMATION FOR SEQUENCE IDENTIFICATION NUMBER: 74:
(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 21
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear
(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 74:

RCTRTCNGCN AGNGANGCYT T 21

(2) INFORMATION FOR SEQUENCE IDENTIFICATION NUMBER: 75:
(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 21
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear
(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 75:

NGARTCNGCY AARCTNGCYT T 21

(2) INFORMATION FOR SEQUENCE IDENTIFICATION NUMBER: 76:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 21
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 76:

NGARTCNGCN AGRCTNGCYT T 21

(2) INFORMATION FOR SEQUENCE IDENTIFICATION NUMBER: 77:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 730
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 77:

GTATGTGTCA GCCATGACCA CCCCGGCTCG TATGTCACCT GTAGATTTC ACACGCCAAG 60
CTCCCCCAAA TCGCCCCCTT CGGAAATGTC TCCACCCGTG TCCAGCATGA CGGTGTCCAT 120
GCCTTCCATG GCGGTCAGCC CCTTCATGGA AGAAGAGAGA CCTCTACTTC TCGTGACACC 180
ACCAAGGCTG CGGGAGAAGA AGTTTGACCA TCACCCTCAG CAGTTCAGCT CCTTCCACCA 240
CAACCCCGCG CATGACAGTA ACAGCCTCCC TGCTAGCCCC TTGAGGATAG TGGAGGATGA 300
GGAGTATGAA ACGACCCAAG AGTACGAGCC AGCCCAAGAG CCTGTTAAGA AACTCGCCAA 360
TAGCCGGCGG GCCAAAAGAA CCAAGCCCAA TGGCCACATT GCTAACAGAT TGGAAGTGGA 420
CAGCAACACA AGCTCCCAGA GCAGTAACTC AGAGAGTGAA ACAGAAGATG AAAGAGTAGG 480
TGAAGATACG CCTTTCCTGG GCATACAGAA CCCCTGGCA GCCAGTCTTG AGGCAACACC 540
TGCCTTCCGC CTGGCTGACA GCAGGACTAA CCCAGCAGGC CGCTTCTCGA CACAGGAAGA 600
AATCCAGGCC AGGCTGTCTA GTGTAATTGC TAACCAAGAC CCTATTGCTG TATAAACCT 660
AAATAAACAC ATAGATTCAC CTGTAAACT TTATTTTATA TAATAAAGTA TTCCACCTTA 720
AATTAAACAA 730

(2) INFORMATION FOR SEQUENCE IDENTIFICATION NUMBER: 78:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 21
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 78:

RCTRTCNGCY AARCTNGCYT T 21

(2) INFORMATION FOR SEQUENCE IDENTIFICATION NUMBER: 79:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 21
- (B) TYPE: nucl ic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 79:

RCTRCTNGCN AGRCTNGCYT T 21

(2) INFORMATION FOR SEQUENCE IDENTIFICATION NUMBER: 80:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 20
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 80:

ACNACNGARA TGGCTCNNGA 20

(2) INFORMATION FOR SEQUENCE IDENTIFICATION NUMBER: 81:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 20
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 81:

ACNACNGARA TGGCAGYNGA 20

(2) INFORMATION FOR SEQUENCE IDENTIFICATION NUMBER: 82:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 20
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 82:

CAYCARGTNT GGGCNGCNAA 20

(2) INFORMATION FOR SEQUENCE IDENTIFICATION NUMBER: 83:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 20
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 83:

TTYGTNGTNA THGARGGNAA 20

(2) INFORMATION FOR SEQUENCE IDENTIFICATION NUMBER: 84:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 20
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 84:

AARGGNGAYG CNCAYACNGA 20

(2) INFORMATION FOR SEQUENCE IDENTIFICATION NUMBER: 85:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 20
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 85:

GARGCNYTNG CNGCNYTNAA 20

(2) INFORMATION FOR SEQUENCE IDENTIFICATION NUMBER: 86:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 20
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 86:

GTNGGNTCNG TNCARGARYT 20

(2) INFORMATION FOR SEQUENCE IDENTIFICATION NUMBER: 87:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 20
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 87:

GTNGGNAGYG TNCARGARYT 20

(2) INFORMATION FOR SEQUENCE IDENTIFICATION NUMBER: 88:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 21
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 88:

NACYTTYTTN ARDATYTGNC C 21

(2) INFORMATION FOR SEQUENCE IDENTIFICATION NUMBER: 89:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 417
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ix) FEATURE:

- (D) OTHER INFORMATION: Xaa in positions 14, 23, 90, 100, 126, and 135 is a stop codon.

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 89:

TCTAA AAC TAC AGA GAC TGT ATT TTC ATG ATC ATC ATA GTT CTG TGA AAT ATA 53
Asn Tyr Arg Asp Cys Ile Phe Met Ile Ile Ile Val Leu Xaa Asn Ile
1 5 10 15

CTT AAA CCG CTT TGG TCC TGA TCT TGT AGG AAG TCA GAA CTT CGC ATT 101
Leu Lys Pro Leu Trp Ser Xaa Ser Cys Arg Lys Ser Glu Leu Arg Ile
20 25 30

AGC AAA GCG TCA CTG GCT GAT TCT GGA GAA TAT ATG TGC AAA GTG ATC 149
Ser Lys Ala Ser Leu Ala Asp Ser Gly Glu Ser Met Cys Lys Val Ile
35 40 45

AGC	AAA	CTA	GGA	AAT	GAC	AGT	GCC	TCT	GCC	AAC	ATC	ACC	ATT	GTG	GAG	197
Ser	Lys	Leu	Gly	Asn	Asp	Ser	Ala	Ser	Ala	Asn	Ile	Arg	Ile	Val	Glu	
50						55					60					
TCA	AAC	GGT	AAG	AGA	TGC	CTA	CTG	CGT	GCT	ATT	TCT	CAG	TCT	CTA	AGA	245
Ser	Asn	Gly	Lys	Arg	Cys	Leu	Leu	Arg	Ala	Il	Ser	Gln	Ser	Leu	Arg	
65					70					75					80	
GGA	GTG	ATC	AAG	GTA	TGT	GGT	CAC	ACT	TGA	ATC	ACG	CAG	GTG	TGT	GAA	293
Gly	Val	Ile	Lys	Val	Cys	Gly	His	Thr	Xaa	Ile	Thr	Gln	Val	Cys	Glu	
				85					90					95		
ATC	TCA	TTG	TGA	ACA	AAT	AAA	AAT	CAT	GAA	AGG	AAA	ACT	CTA	TGT	TTG	341
Il	Ser	Cys	Xaa	Thr	Asn	Lys	Asn	His	Glu	Arg	Lys	Thr	Leu	Cys	Leu	
			100					105						110		
AAA	TAT	CTT	ATG	GGT	CCT	CCT	GTA	AAG	CTC	TTC	ACT	CCA	TAA	GGT	GAA	389
Lys	Tyr	Leu	Met	Gly	Pro	Pro	Val	Lys	Leu	Phe	Thr	Pro	Xaa	Gly	Glu	
		115					120					125				
ATA	GAC	CTG	AAA	TAT	ATA	TAG	ATT	ATT	T							417
Ile	Asp	Leu	Lys	Tyr	Ile	Xaa	Ile	Ile								
130						135										

- (2) INFORMATION FOR SEQUENCE IDENTIFICATION NUMBER: 90:
- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 33
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear
 - (ix) FEATURE:
 - (D) OTHER INFORMATION: N at positions 19, 25, and 31 is Inosine.
Y can be cytidine or thymidine.
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 90:

CCGAATTCTG CAGGARACNC ARCCNGAYCC NGG 33

(2) INFORMATION FOR SEQUENCE IDENTIFICATION NUMBER: 91:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 37
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear
- (ix) FEATURE:
 - (D) OTHER INFORMATION: N at positions 14, 20, 23, 29, and 35 is Inosine.
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 91:

AAGGATCCTG CAGNGTRTAN GCNCCDATNA CCATNGG

37

(2) INFORMATION FOR SEQUENCE IDENTIFICATION NUMBER: 92:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 34
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear
- (ix) FEATURE:
 - (D) OTHER INFORMATION: N at positions 16, 21, and 24 is Inosine. Y can be cytidine or thymidine.
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 92:

CCGAATTCTG CAGGCNGAYT CNGGNGARTA YATG 34

(2) INFORMATION FOR SEQUENCE IDENTIFICATION NUMBER: 93:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 33
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear
- (ix) FEATURE:
 - (D) OTHER INFORMATION: N at positions 16 and 25 is Inosine. Y can be cytidine or thymidine.
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 93:

CCGAATTCTG CAGGCNGAYA GYGGNGARTA YAT 33

(2) INFORMATION FOR SEQUENCE IDENTIFICATION NUMBER: 94:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 34
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ix) FEATURE:

- (D) OTHER INFORMATION: N at positions 14, 15, 16, 26, and 29 is Inosine. Y can be cytidine or thymidine.

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 94:

AAGGATCCTG CAGNNNCATR TAYTCNCCNG ARTC 34

(2) INFORMATION FOR SEQUENCE IDENTIFICATION NUMBER: 95:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 34
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ix) FEATURE:

- (D) OTHER INFORMATION: N at positions 14, 15, 16, and 26 is Inosine. Y can be cytidine or thymidine.

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 95:

AAGGATCCTG CAGNNNCATR TAYTCNCCRC TRTC 34

(2) INFORMATION FOR SEQUENCE IDENTIFICATION NUMBER: 96:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 33
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ix) FEATURE:

- (D) OTHER INFORMATION: N at positions 21, 28, and 31 is Inosine. Y can be cytidine or thymidine.

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 96:

CCGAATTCTG CAGCAYCARG TNTGGGCNGC NAA 33

(2) INFORMATION FOR SEQUENCE IDENTIFICATION NUMBER: 97:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 35
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ix) FEATURE:

- (D) OTHER INFORMATION: N at position 31 is Inosine. Y can be cytidine or thymidine.

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 97:

CCGAATTCTG CAGATHTTYT TYATGGARCC NGARG 35

(2) INFORMATION FOR SEQUENCE IDENTIFICATION NUMBER: 98:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 35
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ix) FEATURE:

- (D) OTHER INFORMATION: N at positions 18, 21, 24, 27, and 33 is Inosine. Y can be cytidine or thymidine.

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 98:

CCGAATTCTG CAGGGGGNCC NCCNGCNTTY CCNGT 35

(2) INFORMATION FOR SEQUENCE IDENTIFICATION NUMBER: 99:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 33
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ix) FEATURE:

- (D) OTHER INFORMATION: N at positions 21 and 24 is Inosin . Y can be cytidine or thymidine.

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 99:

CCGAATTCTG CAGTGGTTYG TNGTNATHGA RGG 33

(2) INFORMATION FOR SEQUENCE IDENTIFICATION NUMBER: 100:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 35
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ix) FEATURE:

- (D) OTHER INFORMATION: N at positions 17, 20, and 26 is Inosine.
Y can be cytidine or thymidine.

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 100:

AAGGATCCTG CAGYTTNGCU NGCCCANACY TGRTG 35

(2) INFORMATION FOR SEQUENCE IDENTIFICATION NUMBER: 101:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 33
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ix) FEATURE:

- (D) OTHER INFORMATION: N at position 19 is Inosine. Y can be
cytidine or thymidine.

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 101:

AAGGATCCTG CAGGCYTCNG GYTCCATRAA RAA 33

(2) INFORMATION FOR SEQUENCE IDENTIFICATION NUMBER: 102:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 33
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ix) FEATURE:

- (D) OTHER INFORMATION: N at positions 16, 22, 25, 28, and 31 is
Inosine.

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 102:

AAGGATCCTG CAGACNGGRA ANGCNGGNGG NCC 33

(2) INFORMATION FOR SEQUENCE IDENTIFICATION NUMBER: 103:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 35
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ix) FEATURE:

- (D) OTHER INFORMATION: N at positions 17, 26, and 29 is Inosine.
Y can be cytidine or thymidine.

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 103:

AAGGATCCTG CAGYTTNCCY TCDATNACNA CRAAC 35

(2) INFORMATION FOR SEQUENCE IDENTIFICATION NUMBER: 104:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 33
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ix) FEATURE:

- (D) OTHER INFORMATION: N at position 18 is Inosine. Y can be
cytidine or thymidine.

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 104:

CATRTAYTCR TAYTCTCNGC AAGGATCCTG CAG 33

(2) INFORMATION FOR SEQUENCE IDENTIFICATION NUMBER: 105:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 33
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ix) FEATURE:

- (D) OTHER INFORMATION: N at position 19, 25, and 31 is Inosine.
Y can be cytidine or thymidine.

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 105:

CCGAATTCTG CAGAARGGNG AYGCNCAYAC NGA 33

(2) INFORMATION FOR SEQUENCE IDENTIFICATION NUMBER: 106:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 33
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ix) FEATURE:

- (D) OTHER INFORMATION: N at position 3 and 18 is Inosine. Y can be cytidine or thymidine.

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 106:

GCNGCYAANG CYTCYTTNGC AAGGATCCTG CAG 33

(2) INFORMATION FOR SEQUENCE IDENTIFICATION NUMBER: 107:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 33
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ix) FEATURE:

- (D) OTHER INFORMATION: N at position 3, 6, 9, and 18 is Inosine. Y can be cytidine or thymidine.

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 107:

GCNGCNAGNG CYTCYTTNGC AAGGATCCTG CAG 33

(2) INFORMATION FOR SEQUENCE IDENTIFICATION NUMBER: 108:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 30
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ix) FEATURE:

- (D) OTHER INFORMATION: N at position 3, 12, and 15 is Inosine. Y can be cytidine or thymidine.

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 108:

TCNGCRAART ANCCNGCAAG GATCCTGCAG 30

(2) INFORMATION FOR SEQUENCE IDENTIFICATION NUMBER: 109:
(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 38
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear
(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 109:

CATCGATCTG CAGGCTGATT CTGGAGAATA TATGTGCA 38

(2) INFORMATION FOR SEQUENCE IDENTIFICATION NUMBER: 110:
(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 37
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear
(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 110:

AAGGATCCTG CAGCCACATC TCGAGTCGAC ATCGATT 37

(2) INFORMATION FOR SEQUENCE IDENTIFICATION NUMBER: 111:
(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 37
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear
(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 111:

CCGAATTCTG CAGTGATCAG CAAACTAGGA AATGACA 37

(2) INFORMATION FOR SEQUENCE IDENTIFICATION NUMBER: 112:
(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 37
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear
(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 112:

CATCGATCTG CAGCCTAGTT TGCTGATCAC TTTGCAC 37

- (2) INFORMATION FOR SEQUENCE IDENTIFICATION NUMBER: 113:
(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 37
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear
(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 113:

AAGGATCCTG CAGTATATTC TCCAGAATCA GCCAGTG 37

- (2) INFORMATION FOR SEQUENCE IDENTIFICATION NUMBER: 114:
(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 34
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear
(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 114:

AAGGATCCTG CAGGCACGCA GTAGGCATCT CTTA 34

- (2) INFORMATION FOR SEQUENCE IDENTIFICATION NUMBER: 115:
(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 35
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear
(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 115:

CCGAATTCTG CAGCAGAACT TCGCATTAGC AAAGC 35

- (2) INFORMATION FOR SEQUENCE IDENTIFICATION NUMBER: 116:
(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 33
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear
(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 116:

CATCCCGGGA TGAAGAGTCA GGAGTCTGTG GCA 33

- (2) INFORMATION FOR SEQUENCE IDENTIFICATION NUMBER: 117:
(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 39
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: singl
 (D) TOPOLOGY: linear
(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 117:

ATACCCGGGC TGCAGACAAT GAGATTTAC ACACCTGCG 39

- (2) INFORMATION FOR SEQUENCE IDENTIFICATION NUMBER: 118:
(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 36
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear
(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 118:

AAGGATCCTG CAGTTTGGAA CCTGCCACAG ACTCCT 36

- (2) INFORMATION FOR SEQUENCE IDENTIFICATION NUMBER: 119:
(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 39
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear
(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 119:

ATACCCGGGC TGCAGATGAG ATTTACACA CCTGCGTGA 39

- (2) INFORMATION FOR SEQUENCE IDENTIFICATION NUMBER: 120:
(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 12
 (B) TYPE: amino acid
 (C) STRANDEDNESS:
 (D) TOPOLOGY: linear
(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 120:

His Gln Val Trp Ala Ala Lys Ala Ala Gly Leu Lys
1 5 10

(2) INFORMATION FOR SEQUENCE IDENTIFICATION NUMBER: 121:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 16
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 121:

Gly Gly Leu Lys Lys Asp Ser Leu Leu Thr Val Arg Leu Gly Ala Asn
1 5 10 15

(2) INFORMATION FOR SEQUENCE IDENTIFICATION NUMBER: 122:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 13
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ix) FEATURE:

(D) OTHER INFORMATION: Xaa in position 12 is unknown.

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 122:

Leu Gly Ala Trp Gly Pro Pro Ala Phe Pro Val Xaa Tyr
1 5 10

(2) INFORMATION FOR SEQUENCE IDENTIFICATION NUMBER: 123:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 23
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 123:

Leu Leu Thr Val Arg Leu Gly Ala Trp Gly His Pro Ala Phe Pro Ser
1 5 10 15

Cys Gly Arg Leu Lys Glu Asp
20

(2) INFORMATION FOR SEQUENCE IDENTIFICATION NUMBER: 124:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 13

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(ix) **FEATURE:**

(D) OTHER INFORMATION: Xaa in position 10 is unknown.

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 124:

Tyr Ile Phe Phe Met Glu Pro Glu Ala Xaa Ser Ser Gly
1 5 10

(2) INFORMATION FOR SEQUENCE IDENTIFICATION NUMBER: 125:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 23

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 125:

Lys Glu Asp Ser Arg Tyr Ile Phe Phe Met Glu Pro Glu Ala Asn Ser
1 5 10 15

Ser Gly Gly Pro Gly Arg Leu
20

(2) INFORMATION FOR SEQUENCE IDENTIFICATION NUMBER: 126:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 14

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 126:

Val Ala Gly Ser Lys Leu Val Leu Arg Cys Glu Thr Ser Ser
1 5 10

(2) INFORMATION FOR SEQUENCE IDENTIFICATION NUMBER: 127:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 16
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 127:

Glu Tyr Lys Cys Leu Lys Phe Lys Trp Phe Lys Lys Ala Thr Val Met
1 5 10 15

(2) INFORMATION FOR SEQUENCE IDENTIFICATION NUMBER: 128:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 26
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 128:

Cys Glu Thr Ser Ser Glu Tyr Ser Ser Leu Lys Phe Lys Trp Phe Lys
1 5 10 15

Asn Gly Ser Glu Leu Ser Arg Lys Asn Lys
20 25

(2) INFORMATION FOR SEQUENCE IDENTIFICATION NUMBER: 129:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 13
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ix) FEATURE:

(D) OTHER INFORMATION: Xaa in position 12 is unknown.

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 129:

Lys Ala Ser Leu Ala Asp Ser Gly Glu Tyr Met Xaa Lys
1 5 10

(2) INFORMATION FOR SEQUENCE IDENTIFICATION NUMBER: 130:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 23
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 130:

Glu Leu Arg Ile Ser Lys Ala Ser Leu Ala Asp Ser Gly Glu Tyr Met
1 5 10 15
Cys Lys Val Ile Ser Lys Leu
20

(2) INFORMATION FOR SEQUENCE IDENTIFICATION NUMBER: 131:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 12
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 131:

Ala Ser Leu Ala Asp Glu Tyr Glu Tyr Met Arg Lys
1 5 10

(2) INFORMATION FOR SEQUENCE IDENTIFICATION NUMBER: 132:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 22
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 132:

L u Arg Ile Ser Lys Ala Ser Leu Ala Asp Ser Gly Glu Tyr Met Cys
1 5 10 15
Lys Val Ile Ser Lys Leu
20

(2) INFORMATION FOR SEQUENCE IDENTIFICATION NUMBER: 133:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 744
(B) TYPE: nucleic acid
(C) STRANDEDNESS: singl
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 133:

CCTGCAG	CAT	CAA	GTG	TGG	GCG	GCG	AAA	GCC	GGG	GGC	TTG	AAG	AAG	GAC	TCG	CTG	55
	His	Gln	Val	Trp	Ala	Ala	Lys	Ala	Gly	Gly	Leu	Lys	Lys	Asp	Ser	Leu	
	1				5				10						15		
CTC	ACC	GTG	CGC	CTG	GGC	GCC	TGG	GGC	CAC	CCC	GCC	TTC	CCC	TCC	TGC		103
Leu	Thr	Val	Arg	Leu	Gly	Ala	Trp	Gly	His	Pro	Ala	Phe	Pro	Ser	Cys		
		20					25						30				
GGG	CGC	CTC	AAG	GAG	GAC	AGC	AGG	TAC	ATC	TTC	TTC	ATG	GAG	CCC	GAG		151
Gly	Arg	Leu	Lys	Glu	Asp	Ser	Arg	Tyr	Ile	Phe	Phe	Met	Glu	Pro	Glu		
	35						40					45					
GCC	AAC	AGC	AGC	GGC	GGG	CCC	GGC	CGC	CTT	CCG	AGC	CTC	CTT	CCC	CCC		199
Ala	Asn	Ser	Ser	Gly	Gly	Pro	Gly	Arg	Leu	Pro	Ser	Leu	Leu	Pro	Pro		
	50					55					60						
TCT	CGA	GAC	GGG	CCG	GAA	CCT	CAA	GAA	GGA	GGT	CAG	CCG	GGT	GCT	GTG		247
Ser	Arg	Asp	Gly	Pro	Glu	Pro	Gln	Glu	Gly	Gly	Gln	Pro	Gly	Ala	Val		
	65				70				75						80		
CAA	CGG	TGC	GCC	TTG	CCT	CCC	CGC	TTG	AAA	GAG	ATG	AAG	AGT	CAG	GAG		295
Gln	Arg	Cys	Ala	Leu	Pro	Pro	Arg	Leu	Lys	Glu	Met	Lys	Ser	Gln	Glu		
			85					90						95			
TCT	GTG	GCA	GGT	TCC	AAA	CTA	GTG	CTT	CGG	TGC	GAG	ACC	AGT	TCT	GAA		343
Ser	Val	Ala	Gly	Ser	Lys	Leu	Val	Leu	Arg	Cys	Glu	Thr	Ser	Ser	Glu		
		100					105						110				
TAC	TCC	TCT	CTC	AAG	TTC	AAG	TGG	TTC	AAG	AAT	GGG	AGT	GAA	TTA	AGC		391
Tyr	Ser	Ser	Leu	Lys	Phe	Lys	Trp	Phe	Lys	Asn	Gly	Ser	Glu	Leu	Ser		
		115					120					125					
CGA	AAG	AAC	AAA	CCA	GAA	AAC	ATC	AAG	ATA	CAG	AAA	AGG	CCG	GGG	AAG		439
Arg	Lys	Asn	Lys	Pro	Glu	Asn	Ile	Lys	Ile	Gln	Lys	Arg	Pro	Gly	Lys		
	130					135					140						
TCA	GAA	CTT	CGC	ATT	AGC	AAA	GCG	TCA	CTG	GCT	GAT	TCT	GGA	GAA	TAT		487
Ser	Glu	Leu	Arg	Ile	Ser	Lys	Ala	Ser	Leu	Ala	Asp	Ser	Gly	Glu	Tyr		
	145				150					155					160		
ATG	TGC	AAA	GTG	ATC	AGC	AAA	CTA	GGA	AAT	GAC	AGT	GCC	TCT	GCC	AAC		535
Met	Cys	Lys	Val	Ile	Ser	Lys	Leu	Gly	Asn	Asp	Ser	Ala	Ser	Ala	Asn		
				165					170					175			

ATC ACC ATT GTG GAG TCA AAC GGT AAG AGA TGC CTA CTG CGT GCT ATT	583
Ile Thr Ile Val Glu Ser Asn Gly Lys Arg Cys L u L u Arg Ala Il	
180 185 190	
TCT CAG TCT CTA AGA GGA GTG ATC AAG GTA TGT GGT CAC ACT	625
Ser Gln Ser Leu Arg Gly Val Ile Lys Val Cys Gly His Thr	
195 200 205	
TGAATCACGC AGGTGTGTGA AATCTCATTG TGAACAAATA AAAATCATGA AAGGAAAAAA	685
AAAAAAAAAA AATCGATGTC GACTCGAGAT GTGGCTGCAG GTCGACTCTA GAGGATCCC	744

(2) INFORMATION FOR SEQUENCE IDENTIFICATION NUMBER: 134:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1193
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 134:

CCTGCAG CAT CAA GTG TGG GCG GCG AAA GCC GGG GGC TTG AAG AAG GAC TCG CTG	55
His Gln Val Trp Ala Ala Lys Ala Gly Gly Leu Lys Lys Asp Ser Leu	
1 5 10 15	
CTC ACC GTG CGC CTG GGC GCC TGG GGC CAC CCC GCC TTC CCC TCC TGC	103
Leu Thr Val Arg Leu Gly Ala Trp Gly His Pro Ala Phe Pro Ser Cys	
20 25 30	
GGG CGC CTC AAG GAG GAC AGC AGG TAC ATC TTC TTC ATG GAG CCC GAG	151
Gly Arg Leu Lys Glu Asp Ser Arg Tyr Ile Phe Phe Met Glu Pro Glu	
35 40 45	
GCC AAC AGC AGC GGC GGG CCC GGC CGC CTT CCG AGC CTC CTT CCC CCC	199
Ala Lys Ser Ser Gly Gly Pro Gly Arg Leu Pro Ser Leu Leu Pro Pro	
50 55 60	
TCT CGA GAC GGG CCG GAA CCT CAA GAA GGA GGT CAG CCG GGT GCT GTG	247
Ser Arg Asp Gly Pro Glu Pro Gln Glu Gly Gly Gln Pro Gly Ala Val	
65 70 75 80	
CAA CGG TGC GCC TTG CCT CCC CGC TTG AAA GAG ATG AAG AGT CAG GAG	295
Gln Arg Cys Ala Leu Pro Pro Arg Leu Lys Glu Met Lys Ser Gln Glu	
85 90 95	
TCT GTG GCA GGT TCC AAA CTA GTG CTT CGG TGC GAG ACC AGT TCT GAA	343
Ser Val Ala Gly Ser Lys Leu Val Leu Arg Cys Glu Thr Ser Ser Glu	
100 105 110	

(2) INFORMATION FOR SEQUENCE IDENTIFICATION NUMBER: 135:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1108
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 135:

CCTGCAG	CAT	CAA	GTG	TGG	GCG	GCG	AAA	GCC	GGG	GGC	TTG	AAG	AAG	GAC	TCG	CTG	55
	His	Gln	Val	Trp	Ala	Ala	Lys	Ala	Gly	Gly	Leu	Lys	Lys	Asp	Ser	Leu	
	1				5					10					15		
CTC	ACC	GTG	CGC	CTG	GGC	GCC	TGG	GGC	CAC	CCC	GCC	TTC	CCC	TCC	TGC		103
L u	Thr	Val	Arg	Leu	Gly	Ala	Trp	Gly	His	Pro	Ala	Phe	Pro	Ser	Cys		
		20					25					30					
GGG	CGC	CTC	AAG	GAG	GAC	AGC	AGG	TAC	ATC	TTC	TTC	ATG	GAG	CCC	GAG		151
Gly	Arg	Leu	Lys	Glu	Asp	Ser	Arg	Tyr	Ile	Phe	Phe	Met	Glu	Pro	Glu		
		35					40					45					
GCC	AAC	AGC	AGC	GGC	GGG	CCC	GGC	CGC	CTT	CCG	AGC	CTC	CTT	CCC	CCC		199
Ala	Asn	Ser	Ser	Gly	Gly	Pro	Gly	Arg	Leu	Pro	Ser	Leu	Leu	Pro	Pro		
	50					55					60						
TCT	CGA	GAC	GGG	CCG	GAA	CCT	CAA	GAA	GGA	GGT	CAG	CCG	GGT	GCT	GTG		247
Ser	Arg	Asp	Gly	Pro	Glu	Pro	Gln	Glu	Gly	Gly	Gln	Pro	Gly	Ala	Val		
	65				70				75						80		
CAA	CGG	TGC	GCC	TTG	CCT	CCC	CGC	TTG	AAA	GAG	ATG	AAG	AGT	CAG	GAG		295
Gln	Arg	Cys	Ala	Leu	Pro	Pro	Arg	Leu	Lys	Glu	Met	Lys	Ser	Gln	Glu		
			85					90						95			
TCT	GTG	GCA	GGT	TCC	AAA	CTA	GTG	CTT	CGG	TGC	GAG	ACC	AGT	TCT	GAA		343
Ser	Val	Ala	Gly	Ser	Lys	Leu	Val	Leu	Arg	Cys	Glu	Thr	Ser	Ser	Glu		
		100					105						110				
TAC	TCC	TCT	CTC	AAG	TTC	AAG	TGG	TTC	AAG	AAT	GGG	AGT	GAA	TTA	AGC		391
Tyr	Ser	Ser	Leu	Lys	Phe	Lys	Trp	Phe	Lys	Asn	Gly	Ser	Glu	Leu	Ser		
		115					120					125					
CGA	AAG	AAC	AAA	CCA	GAA	AAC	ATC	AAG	ATA	CAG	AAA	AGG	CCG	GGG	AAG		439
Arg	Lys	Asn	Lys	Pro	Glu	Asn	Ile	Lys	Ile	Gln	Lys	Arg	Pro	Pro	Lys		
	130					135					140						
TCA	GAA	CTT	CGC	ATT	AGC	AAA	GCG	TCA	CTG	GCT	GAT	TCT	GGA	GAA	TAT		487
Ser	Glu	Leu	Arg	Ile	Ser	Lys	Ala	Ser	Leu	Ala	Asp	Ser	Gly	Glu	Tyr		
	145				150				155						160		
ATG	TGC	AAA	GTG	ATC	AGC	AAA	CTA	GGA	AAT	GAC	AGT	GCC	TCT	GCC	AAC		535
Met	Cys	Lys	Val	Ile	Ser	Lys	Leu	Gly	Asn	Asp	Ser	Ala	Ser	Ala	Asn		
				165				170						175			

ATC	ACC	ATT	GTG	GAG	TCA	AAC	GCC	ACA	TCC	ACA	TCT	ACA	GCT	GGG	ACA	583
Ile	Arg	Ile	Val	Glu	Ser	Asn	Ala	Thr	Ser	Thr	Ser	Thr	Ala	Gly	Thr	
			180					185					190			

AGC	CAT	CTT	GTC	AAG	TGT	GCA	GAG	AAG	GAG	AAA	ACT	TTC	TGT	GTG	AAT	631
Ser	His	Leu	Val	Lys	Cys	Ala	Glu	Lys	Glu	Lys	Thr	Phe	Cys	Val	Asn	
		195					200					205				

GGA	GGC	GAG	TGC	TTC	ATG	GTG	AAA	GAC	CTT	TCA	AAT	CCC	TCA	AGA	TAC	679
Gly	Gly	Glu	Cys	Phe	Met	Val	Lys	Asp	Leu	Ser	Asn	Pro	Ser	Arg	Tyr	
	210					215					220					

TTG	TGC	AAG	TGC	CCA	AAT	GAG	TTT	ACT	GGT	GAT	CGC	TGC	CAA	AAC	TAC	727
L u	Cys	Lys	Cys	Pro	Asn	Glu	Phe	Thr	Gly	Asp	Arg	Cys	Gln	Asn	Tyr	
225					230				235						240	

GTA	ATG	GCC	AGC	TTC	TAC	AGT	ACG	TCC	ACT	CCC	TTT	CTG	TCT	CTG	CCT	775
Val	Met	Ala	Ser	Phe	Tyr	Ser	Thr	Ser	Thr	Pro	Phe	Leu	Ser	Leu	Pro	
			245					250						255		

GAA	TAGCGCATCT	CAGTCGGTGC	CGCTTTCTTG	TTGCCGCATC	TCCCCTCAGA	TTCCGCCTAG	838
Glu							

DAGCTAGATGC	GTTTTACCAG	GTCTAACATT	GA CTGCCTCT	GCCTGTCGCA	TGAGAACATT	898
GAACACAAGCG	ATTGTATGAC	TTCCTCTGTC	CGTGACTAGT	GGGCTCTGAG	CTACTCGTAG	958
GTGCGTAAGG	CTCCAGTGTT	TCTGAAATTG	ATCTTGAATT	ACTGTGATAC	GACATGATAG	1018
TCCCCTCTCAC	CCAGTGCAAT	GACAATAAAG	GCCTTGAAAA	GTCAAAAAAA	AAAAAAAAAA	1078
AAAAATCGAT	GTCGACTCGA	GATGTGGCTG				1108

(2) INFORMATION FOR SEQUENCE IDENTIFICATION NUMBER: 136:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 559
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ix) FEATURE:

- (D) OTHER INFORMATION: N in position 214 is unknown.

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 136:

AGTTTCCCCC	CCCAACTTGT	CGGAACTCTG	GGCTCGCGCG	CAGGGCAGGA	GCGGAGCGGC	60
GGCGGCTGCC	CAGGCGATGC	GAGCGCGGGC	CGGACGGTAA	TCGCCTCTCC	CTCCTCGGGC	120
TGCGAGCGCG	CCGGACCGAG	GCAGCGACAG	GAGCGGACCG	CGGCGGGAAC	CGAGGACTCC	180
CCAGCGGCGC	GCCAGCAGGA	GCCACCCCGC	GAGNCGTGCG	ACCGGGACGG	AGCGCCCGCC	240
AGTCCCAGGT	GGCCCGGACC	GCACGTTGCG	TCCCCGCGCT	CCCCGCCGGC	GACAGGAGAC	300
GCTCCCCCCC	ACGCCGCGCG	CGCCTCGGCC	CGGTCGCTGG	CCCGCCTCCA	CTCCGGGGAC	360
AAACTTTTCC	CGAAGCCGAT	CCCAGCCCTC	GGACCCAAAC	TTGTCGCGCG	TCGCCTTCGC	420
CGGGAGCCGT	CCGCGCAGAG	CGTGCACTTC	TCGGGCGAG	ATG TCG GAG	CGC AGA	474
				Met Ser Glu Arg Arg		
				1	5	

GAA GGC AAA GGC AAG GGG AAG GGC GGC AAG AAG GAC CGA GGC TCC GGG	522
Glu Gly Lys Gly Lys Gly Lys Gly Gly Lys Lys Asp Arg Gly Ser Gly	
10 15 20	

AAG AAG CCC GTG CCC GCG GCT GGC GGC CCG AGC CCA G	559
Lys Lys Pro Val Pro Ala Ala Gly Gly Pro Ser Pro Ala	
25 30	

(2) INFORMATION FOR SEQUENCE IDENTIFICATION NUMBER: 137:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 252
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ix) FEATURE:

- (D) OTHER INFORMATION: N in position 8 could be either A or G.

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 137:

CC CAT CAN GTG TGG GCG GCG AAA GCC GGG GGC TTG AAG AAG GAC TCG	47
His Gln Val Trp Ala Ala Lys Ala Gly Gly Leu Lys Lys Asp Ser	
1 5 10 15	
CTG CTC ACC GTG CGC CTG GGC GCC TGG GGC CAC CCC GCC TTC CCC TCC	95
Leu Leu Thr Val Arg Leu Gly Ala Trp Gly His Pro Ala Phe Pro Ser	
20 25 30	
TGC GGG CGC CTC AAG GAG GAC AGC AGG TAC ATC TTC TTC ATG GAG CCC	143
Cys Gly Arg Leu Lys Glu Asp Ser Arg Tyr Ile Phe Phe Met Glu Pro	
35 40 45	
GAG GCC AAC AGC AGC GGC GGG CCC GGC CGC CTT CCG AGC CTC CTT CCC	191
Glu Ala Asn Ser Ser Gly Gly Pro Gly Arg Leu Pro Ser Leu Leu Pro	
50 55 60	
CCC TCT CGA GAC GGG CCG GAA CCT CAA GAA GGA GGT CAG CCG GGT GCT	239
Pro Ser Arg Asp Gly Pro Glu Pro Gln Glu Gly Gly Gln Pro Gly Ala	
65 70 75	
GTG CAA CGG TGC G	252
Val Gln Arg Cys	
80	

95220T "6T09E280

(2) INFORMATION FOR SEQUENCE IDENTIFICATION NUMBER: 138:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 178
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 138:

CCT TGC CTC CCC GCT TGA AAG AGA TGA AGA GTC AGG AGT CTG TGG CAG	48
Leu Pro Pro Arg Leu Lys Glu His Lys Ser Gln Glu Ser Val Ala Gly	
1 5 10 15	
GTT CCA AAC TAG TGC TTC GGT GCG AGA CCA GTT CTG AAT ACT CCT CTC	96
Ser Lys Leu Val Leu Arg Cys Glu Thr Ser Ser Glu Tyr Ser Ser Leu	
20 25 30	
TCA AGT TCA AGT GGT TCA AGA ATG GGA GTG AAT TAA GCC GAA AGA ACA	144
Lys Phe Lys Trp Phe Lys Asn Gly Ser Glu Leu Ser Arg Lys Asn Lys	
35 40 45	
AAC CAC AAA ACA TCA AGA TAC AGA AAA GGC CGG G	178
Pro Gly Asn Ile Lys Ile Gln Lys Arg Pro Gly	
50 55	

(2) INFORMATION FOR SEQUENCE IDENTIFICATION NUMBER: 139:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 122
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 139:

G AAG TCA GAA CTT CGC ATT AGC AAA GCG TCA CTG GCT GAT TCT GGA	46
Lys Ser Glu Leu Arg Ile Ser Lys Ala Ser Leu Ala Asp Ser Gly	
1 5 10 15	
GAA TAT ATG TGC AAA GTG ATC AGC AAA CTA GGA AAT GAC AGT GCC TCT	94
Glu Tyr Met Cys Lys Val Ile Ser Lys Leu Gly Asn Asp Ser Ala Ser	
20 25 30	
GCC AAC ATC ACC ATT GTG GAG TCA AAC G	122
Ala Asn Ile Thr Ile Val Glu Ser Asn Ala	
35	

(2) INFORMATION FOR SEQUENCE IDENTIFICATION NUMBER: 140:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 417
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 140:

TCTAAACTA CAGAGACTGT ATTTTCATGA TCATCATAGT TCTGTGAAAT ATACTTAAAC 60
CGCTTTGGTC CTGATCTTGT AGG AAG TCA GAA CTT CGC ATT AGC AAA GCG 110
Lys Ser Glu Leu Arg Ile Ser Lys Ala
1 5

TCA CTG GCT GAT TCT GGA GAA TAT ATG TGC AAA GTG ATC AGC AAA CTA 158
Ser Leu Ala Asp Ser Gly Glu Tyr Met Cys Lys Val Ile Ser Lys Leu
10 15 20 25

GGA AAT GAC AGT GCC TCT GCC AAC ATC ACC ATT GTG GAG TCA AAC GGT 206
Gly Asn Asp Ser Ala Ser Ala Asn Ile Thr Ile Val Glu Ser Asn Gly
30 35 40

AAG AGA TGC CTA CTG CGT GCT ATT TCT CAG TCT CTA AGA GGA GTG ATC 254
Lys Arg Cys Leu Leu Arg Ala Ile Ser Gln Ser Leu Arg Gly Val Ile
45 50 55

AAG GTA TGT GGT CAC ACT TGAATCACGC AGGTGTGTGA AATCTCATTG 302
Lys Val Cys Gly His Thr
60

TGAACAAATA AAAATCATGA AAGGAAACT CTATGTTTGA AATATCTTAT GGGTCCTCCT 362
GTAAAGCTCT TCACTCCATA AGGTGAAATA GACCTGAAAT ATATATAGAT TATTT 417

(2) INFORMATION FOR SEQUENCE IDENTIFICATION NUMBER: 141:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 102
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 141:

AG ATC ACC ACT GGC ATG CCA GCC TCA ACT GAG ACA GCG TAT GTG TCT 47
Glu Ile Thr Thr Gly Met Pro Ala Ser Thr Glu Thr Ala Tyr Val Ser
1 5 10 15

TCA GAG TCT CCC ATT AGA ATA TCA GTA TCA ACA GAA GGA ACA AAT ACT 95
Ser Glu Ser Pro Ile Arg Ile Ser Val Ser Thr Glu Gly Thr Asn Thr
20 25 30

TCT TCA T 102
Ser Ser Ser
35

(2) INFORMATION FOR SEQUENCE IDENTIFICATION NUMBER: 142:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 69
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 142:

AAG TGC CAA CCT GGA TTC ACT GGA GCG AGA TGT ACT GAG AAT GTG CCC 48
Lys Cys Gln Pro Gly Phe Thr Gly Ala Arg Cys Thr Glu Asn Val Pro
1 5 10 15

ATG AAA GTC CAA ACC CAA GAA 69
Met Lys Val Gln Thr Gln Glu
20

(2) INFORMATION FOR SEQUENCE IDENTIFICATION NUMBER: 143:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 60
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 143:

087360 1095280
AAG TGC CCA AAT GAG TTT ACT GGT GAT CGC TGC CAA AAC TAC GTA ATG 48
Lys Cys Pro Asn Glu Phe Thr Gly Asp Arg Cys Gln Asn Tyr Val Met
1 5 10 15

GCC AGC TTC TAC 60
Ala Ser Phe Tyr
20

(2) INFORMATION FOR SEQUENCE IDENTIFICATION NUMBER: 144:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 36
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 144:

AGT ACG TCC ACT CCC TTT CTG TCT CTG CCT GAA TAG 36
Ser Thr Ser Thr Pro Phe Leu Ser Leu Pro Glu
1 5 10

(2) INFORMATION FOR SEQUENCE IDENTIFICATION NUMBER: 145:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 27
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 145:

AAG CAT CTT GGG ATT GAA TTT ATG GAG
Lys His Leu Gly Ile Glu Phe Met Glu
1 5

27

(2) INFORMATION FOR SEQUENCE IDENTIFICATION NUMBER: 146:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 569
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 146:

AAA GCG GAG GAG CTC TAC CAG AAG AGA GTG CTC ACC ATT ACC GGC ATT
Lys Ala Glu Glu Leu Tyr Gln Lys Arg Val Leu Thr Ile Thr Gly Ile
1 5 10 15

48

TGC ATC GCG CTG CTC GTG GTT GGC ATC ATG TGT GTG GTG GTC TAC TGC
Cys Ile Ala Leu Leu Val Val Gly Ile Met Cys Val Val Val Tyr Cys
20 25 30

96

AAA ACC AAG AAA CAA CGG AAA AAG CTT CAT GAC CGG CTT CGG CAG AGC
Lys Thr Lys Lys Gln Arg Lys Lys Leu His Asp Arg Leu Arg Gln Ser
35 40 45

144

CTT CGG TCT GAA AGA AAC ACC ATG ATG AAC GTA GCC AAC GGG CCC CAC
Leu Arg Ser Glu Arg Asn Thr Met Met Asn Val Ala Asn Gly Pro His
50 55 60

192

CAC CCC AAT CCG CCC CCC GAG AAC GTG CAG CTG GTG AAT CAA TAC GTA
His Pro Asn Pro Pro Pro Glu Asn Val Gln Leu Val Asn Gln Tyr Val
65 70 75 80

240

TCT AAA AAT GTC ATC TCT AGC GAG CAT ATT GTT GAG AGA GAG GCG GAG
Ser Lys Asn Val Ile Ser Ser Glu His Ile Val Glu Arg Glu Ala Glu
85 90 95

288

AGC TCT TTT TCC ACC AGT CAC TAC ACT TCG ACA GCT CAT CAT TCC ACT
S r Ser Phe Ser Thr Ser His Tyr Thr Ser Thr Ala His His Ser Thr
100 105 110

336

ACT	GTC	ACT	CAG	ACT	CCC	AGT	CAC	AGC	TGG	AGC	AAT	GGA	CAC	ACT	GAA	384
Thr	Val	Thr	Gln	Thr	Pro	Ser	His	Ser	Trp	Ser	Asn	Gly	His	Thr	Glu	
		115					120					125				
AGC	ATC	ATT	TCG	GAA	AGC	CAC	TCT	GTC	ATC	GTG	ATG	TCA	TCC	GTA	GAA	432
Ser	Ile	Ile	Ser	Glu	Ser	His	Ser	Val	Ile	Val	Met	Ser	Ser	Val	Glu	
	130					135					140					
AAC	AGT	AGG	CAC	AGC	AGC	CCG	ACT	GGG	GGC	CCG	AGA	GGA	CGT	CTC	AAT	480
Asn	Ser	Arg	His	Ser	Ser	Pro	Thr	Gly	Gly	Pro	Arg	Gly	Arg	Leu	Asn	
	145				150					155					160	
GGC	TTG	GGA	GGC	CCT	CGT	GAA	TGT	AAC	AGC	TTC	CTC	AGG	CAT	GCC	AGA	528
Gly	Leu	Gly	Gly	Pro	Arg	Glu	Cys	Asn	Ser	Phe	Leu	Arg	His	Ala	Arg	
				165					170					175		
GAA	ACC	CCT	GAC	TCC	TAC	CGA	GAC	TCT	CCT	CAT	AGT	G	AAAG			569
Glu	Thr	Pro	Asp	Ser	Tyr	Arg	Asp	Ser	Pro	His	Ser					
			180					185								

(2) INFORMATION FOR SEQUENCE IDENTIFICATION NUMBER: 147:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 730
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 147:

G	TAT	GTA	TCA	GCA	ATG	ACC	ACC	CCG	GCT	CGT	ATG	TCA	CCT	GTA	GAT	46
Tyr	Val	Ser	Ala	Met	Thr	Thr	Pro	Ala	Arg	Met	Ser	Pro	Val	Asp		
1					5				10					15		
TTC	CAC	ACG	CCA	AGC	TCC	CCC	AAG	TCA	CCC	CCT	TCG	GAA	ATG	TCC	CCG	94
Phe	His	Thr	Pro	Ser	Ser	Pro	Lys	Ser	Pro	Pro	Ser	Glu	Met	Ser	Pro	
				20					25					30		
CCC	GTG	TCC	AGC	ACG	ACG	GTC	TCC	ATG	CCC	TCC	ATG	GCG	GTC	AGT	CCC	142
Pro	Val	Ser	Ser	Thr	Thr	Val	Ser	Met	Pro	Ser	Met	Ala	Val	Ser	Pro	
			35					40					45			
TTC	GTG	GAA	GAG	GAG	AGA	CCC	CTG	CTC	CTT	GTG	ACG	CCA	CCA	CGG	CTG	190
Phe	Val	Glu	Glu	Glu	Arg	Pro	Leu	Leu	Leu	Val	Thr	Pro	Pro	Arg	Leu	
		50					55					60				
CGG	GAG	AAG	TAT	GAC	CAC	CAC	GCC	CAG	CAA	TTC	AAC	TCG	TTC	CAC	TGC	238
Arg	Glu	Lys	Tyr	Asp	His	His	Ala	Gln	Gln	Phe	Asn	Ser	Phe	His	Cys	
	65					70					75					

AAC Asn 80	CCC Pro	GCG Ala	CAT His	GAG Glu	AGC Ser 85	AAC Asn	AGC Ser	CTG Leu	CCC Pro	CCC Pro 90	AGC Ser	CCC Pro	TTG Leu	AGG Arg	ATA Ile 95	286
GTG Val	GAG Glu	GAT Asp	GAG Glu	GAA Glu 100	TAT Tyr	GAA Glu	ACG Thr	ACC Thr	CAG Gln 105	GAG Glu	TAC Tyr	GAA Glu	CCA Pro	GCT Ala 110	CAA Gln	334
GAG Glu	CCG Pro	GTT Val	AAG Lys 115	AAA Lys	CTC Leu	ACC Thr	AAC Asn	AGC Ser 120	AGC Ser	CGG Arg	CGG Arg	GCC Ala	AAA Lys 125	AGA Arg	ACC Thr	382
AAG Lys	CCC Pro	AAT Asn 130	GGT Gly	CAC His	ATT Ile	GCC Ala	CAC His 135	AGG Arg	TTG Leu	GAA Glu	ATG Met	GAC Asp 140	AAC Asn	AAC Asn	ACA Thr	430
GGC Gly 145	GCT Ala	GAC Asp	AGC Ser	AGT Ser	AAC Asn	TCA Ser 150	GAG Glu	AGC Ser	GAA Glu	ACA Thr	GAG Glu 155	GAT Asp	GAA Glu	AGA Arg	GTA Val	478
GGA Gly 160	GAA Glu	GAT Asp	ACG Thr	CCT Pro	TTC Phe 165	CTG Leu	GCC Ala	ATA Ile	CAG Gln	AAC Asn 170	CCC Pro	CTG Leu	GCA Ala	GCC Ala	AGT Ser 175	526
CTC Leu	GAG Glu	GCG Ala	GCC Ala	CCT Pro 180	GCC Ala	TTC Phe	CGC Arg	CTG Leu	GTC Val 185	GAC Asp	AGC Ser	AGG Arg	ACT Thr	AAC Asn 190	CCA Pro	574
ACA Thr	GGC Gly	GGC Gly	TTC Phe 195	TCT Ser	CCG Pro	CAG Gln	GAA Glu	GAA Glu 200	TTG Leu	CAG Gln	GCC Ala	AGG Arg	CTC Leu 205	TCC Ser	GGT Gly	622
GTA Val	ATC Ile	GCT Ala 210	AAC Asn	CAA Gln	GAC Asp	CCT Pro	ATC Ile 215	GCT Ala	GTC Val	TAA	AACCGAA	ATACACCCAT				672
AGATT	CACCT	GTAAA	ACTTT	ATTTT	TATATA	ATAA	AGTATT	CCACCT	TTAAA	TTAAACAA						730

(2) INFORMATION FOR SEQUENCE IDENTIFICATION NUMBER: 148:

(A) LENGTH: 1652

(C) STRANDEDNESS: single

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 148:

CCAGCGGCGC	GCCAGCAGGA	GCCACCCCGC	GAGCGTGCGA	CCGGGACGGA	GCGCCCGCCA	240
GTCCCAGGTG	GCCCGGACCG	CACGTTGCGT	CCCCGCGCTC	CCCGCCGGCG	ACAGGAGACG	300
CTCCCCCCCCA	CGCCGCGCGC	GCCTCGGCCC	GGTCGCTGGC	CCGCCTCCAC	TCCGGGGACA	360
AACTTTTCCC	GAAGCCGATC	CCAGCCCTCG	GACCCAAACT	TGTCGCGCGT	CGCCTTCGCC	420
GGGAGCCGTC	CGCGCAGAGC	GTGCACTTCT	CGGGCGAG	ATG TCG GAG CGC AGA		473

Met Ser Glu Arg Arg

1

5

GAA GGC AAA GGC AAG GGG AAG GGC GGC AAG AAG GAC CGA GGC TCC GGG	521
Glu Gly Lys Gly Lys Gly Lys Gly Gly Lys Lys Asp Arg Gly Ser Gly	
10 15 20	

AAG AAG CCC GTG CCC GCG GCT GGC GGC CCG AGC CCA GCC TTG CCT CCC	569
Lys Lys Pro Val Pro Ala Ala Gly Gly Pro Ser Pro Ala Leu Pro Pro	
25 30 35	

CGC TTG AAA GAG ATG AAG ATG CAG GAG TCT GTG GCA GGT TCC AAA CTA	617
Arg Leu Lys Glu Met Lys Ser Gln Glu Ser Val Ala Gly Ser Lys Leu	
40 45 50	

GTG CTT CGG TGC GAG ACC AGT TCT GAA TAC TCC TCT CTC AAG TTC AAG	665
Val Leu Arg Cys Glu Thr Ser Ser Glu Tyr Ser Ser Leu Lys Phe Lys	
55 60 65	

GTGG TTC AAG AAT GGG AGT GAA TTA AGC CGA AAG AAC AAA CCA CAA AAC	713
Trp Phe Lys Asn Gly Ser Gly Leu Ser Arg Lys Asn Lys Pro Gln Asn	
70 75 80 85	

ATC AAG ATA CAG AAA AGG CCG GGG AAG TCA GAA CTT CGC ATT AGC AAA	761
Ile Lys Ile Gln Lys Arg Pro Gly Lys Ser Glu Leu Arg Ile Ser Lys	
90 95 100	

GCG TCA CTG GCT GAT TCT GGA GAA TAT ATG TGC AAA GTG ATC AGC AAA	809
Ala Ser Leu Ala Asp Ser Gly Glu Tyr Met Cys Lys Val Ile Ser Lys	
105 110 115	

CTA GGA AAT GAC AGT GCC TCT GCC AAC ATC ACC ATT GTG GAG TCA AAC	857
Leu Gly Asn Asp Ser Ala Ser Ala Asn Ile Thr Ile Val Glu Ser Asn	
120 125 130	

GAG ATC ACC ACT GGC ATG CCA GCC TCA ACT GAG ACA GCG TAT GTG TCT	905
Glu Ile Thr Thr Gly Met Pro Ala Ser Thr Glu Thr Ala Tyr Val Ser	
135 140 145	

TCA GAG TCT CCC ATT AGA ATA TCA GTA TCA ACA GAA GGA ACA AAT ACT	953
Ser Glu Ser Pro Ile Arg Ile Ser Val Ser Thr Glu Gly Thr Asn Thr	
150 155 160 165	

TCT TCA TCC ACA TCC ACA TCT ACA GCT GGG ACA AGC CAT CTT GTC AAG	1001
Ser Ser Ser Thr Ser Thr Ser Thr Ala Gly Thr Ser His Leu Val Lys	
170 175 180	

TGT	GCA	GAG	AAG	GAG	AAA	ACT	TTC	TGT	GTG	AAT	GGA	GGC	GAG	TGC	TTC	1049
Cys	Ala	Glu	Lys	Glu	Lys	Thr	Phe	Cys	Val	Asn	Gly	Gly	Glu	Cys	Phe	
			185					190					195			

ATG	GTG	AAA	GAC	CTT	TCA	AAT	CCC	TCA	AGA	TAC	TTG	TGC	AAG	TGC	CCA	1097
Met	Val	Lys	Asp	Leu	Ser	Asn	Pro	Ser	Arg	Tyr	Leu	Cys	Lys	Cys	Pro	
		200					205					210				

AAT	GAG	TTT	ACT	GGT	GAT	CGC	TGC	CAA	AAC	TAC	GTA	ATG	GCC	AGC	TTC	1145
Asn	Glu	Phe	Thr	Gly	Asp	Arg	Cys	Gln	Asn	Tyr	Val	Met	Ala	Ser	Phe	
		215				220					225					

TAC	AGT	ACG	TCC	ACT	CCC	TTT	CTG	TCT	CTG	CCT	GAA	TAGGCGCATG				1193
Tyr	S	r	Thr	Ser	Thr	Pro	Phe	Leu	Ser	Leu	Pro	Glu				
230					235					240						

CTCAGTCGGT	GCCGCTTTCT	TGTTGCCGCA	TCTCCCCTCA	GATTCAACCT	AGAGCTAGAT	1253
GCGTTTTACC	AGGTCTAACA	TTGACTGCCT	CTGCCTGTCG	CATGAGAACA	TTAACACAAG	1313
CGATTGTATG	ACTTCCTCTG	TCCGTGACTA	GTGGGCTCTG	AGCTACTCGT	AGGTGCGTAA	1373
GGCTCCAGTG	TTTCTGAAAT	TGATCTTGAA	TTACTGTGAT	ACGACATGAT	AGTCCCTCTC	1433
ACCCAGTGCA	ATGACAATAA	AGGCCTTGAA	AAGTCTCACT	TTTATTGAGA	AAATAAAAAAT	1493
CGTTCCACGG	GACAGTCCCT	CTTCTTTATA	AAATGACCCT	ATCCTTGAAA	AGGAGGTGTG	1553
TTAAGTTGTA	ACCAGTACAC	ACTTGAAATG	ATGGTAAGTT	CGCTTCGGTT	CAGAATGTGT	1613
TCTTTCTGAC	AAATAAACAG	AATAAAAAAA	AAAAAAAAAA	A		1652

(2) INFORMATION FOR SEQUENCE IDENTIFICATION NUMBER: 149:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1140
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 149:

CAT	CAN	GTG	TGG	GCG	GCG	AAA	GCC	GGG	GGC	TTG	AAG	AAG	GAC	TCG	CTG	48
His	Gln	Val	Trp	Ala	Ala	Lys	Ala	Gly	Gly	Leu	Lys	Lys	Asp	Ser	Leu	
1				5				10					15			

CTC	ACC	GTG	CGC	CTG	GGC	GCC	TGG	GGC	CAC	CCC	GCC	TTC	CCC	TCC	TGC	96
Leu	Thr	Val	Arg	Leu	Gly	Ala	Trp	Gly	His	Pro	Ala	Phe	Pro	Ser	Cys	
		20					25					30				

GGG	CGC	CTC	AAG	GAG	GAC	AGC	AGG	TAC	ATC	TTC	TTC	ATG	GAG	CCC	GAG	144
Gly	Arg	Leu	Lys	Glu	Asp	Ser	Arg	Tyr	Ile	Phe	Phe	Met	Glu	Pro	Glu	
		35					40					45				

GCC	AAC	AGC	AGC	GGC	GGG	CCC	GGC	CGC	CTT	CCG	AGC	CTC	CTT	CCC	CCC	192
Ala	Asn	Ser	Ser	Gly	Gly	Pro	Gly	Arg	Leu	Pro	Ser	Leu	Leu	Pro	Pro	
		50				55					60					

952220T 6 TGGG 60

TCT Ser 65	CGA Arg	GAC Asp	GGG Gly	CCG Pro	GAA Glu 70	CCT Pro	CAA Gln	GAA Glu	GGA Gly	GGT Gly 75	CAG Gln	CCG Pro	GGT Gly	GCT Ala	GTG Val 80	240
CAA Gln	CGG Arg	TGC Cys	GCC Ala	TTG Leu 85	CCT Pro	CCC Pro	CGC Arg	TTG Leu	AAA Lys 90	GAG Glu	ATG Met	AAG Lys	AGT Ser	CAG Gln 95	GAG Glu	288
TCT Ser	GTG Val	GCA Ala	GGT Gly 100	TCC Ser	AAA Lys	CTA Leu	GTG Val	CTT Leu 105	CGG Arg	TGC Cys	GAG Glu	ACC Thr	AGT Ser 110	TCT Ser	GAA Glu	336
TAC Tyr	TCC Ser	TCT Ser 115	CTC Leu	AAG Lys	TTC Phe	AAG Lys	TGG Trp 120	TTC Phe	AAG Lys	AAT Asn	GGG Gly	AGT Ser 125	GAA Glu	TTA Leu	AGC Ser	384
CGA Arg 130	AAG Lys	AAC Asn	AAA Lys	CCA Pro	GAA Glu	AAC Asn 135	ATC Ile	AAG Lys	ATA Ile	CAG Gln	AAA Lys 140	AGG Arg	CCG Pro	GGG Gly	AAG Lys	432
TCA Ser 145	GAA Glu	CTT Leu	CGC Arg	ATT Ile	AGC Ser 150	AAA Lys	GCG Ala	TCA Ser	CTG Leu	GCT Ala 155	GAT Asp	TCT Ser	GGA Gly	GAA Glu	TAT Tyr 160	480
ATG Met	TGC Cys	AAA Lys	GTG Val	ATC Ile 165	AGC Ser	AAA Lys	CTA Leu	GGA Gly	AAT Asn 170	GAC Asp	AGT Ser	GCC Ala	TCT Ser	GCC Ala 175	AAC Asn	528
ATC Ile	ACC Thr	ATT Ile	GTG Val 180	GAG Glu	TCA Ser	AAC Asn	GCC Ala	ACA Thr 185	TCC Ser	ACA Thr	TCT Ser	ACA Thr	GCT Ala 190	GGG Gly	ACA Thr	576
AGC Ser	CAT His	CTT Leu 195	GTC Val	AAG Lys	TGT Cys	GCA Ala	GAG Glu 200	AAG Lys	GAG Glu	AAA Lys	ACT Thr	TTC Phe 205	TGT Cys	GTG Val	AAT Asn	624
GGA Gly 210	GGC Gly	GAG Glu	TGC Cys	TTC Phe	ATG Met	GTG Val 215	AAA Lys	GAC Asp	CTT Leu	TCA Ser	AAT Asn 220	CCC Pro	TCA Ser	AGA Arg	TAC Tyr	672
TTG Leu 225	TGC Cys	AAG Lys	TGC Cys	CAA Gln	CCT Pro 230	GGA Gly	TTC Phe	ACT Thr	GGA Gly	GCG Ala 235	AGA Arg	TGT Cys	ACT Thr	GAG Glu	AAT Asn 240	720
GTG Val	CCC Pro	ATG Met	AAA Lys	GTC Val 245	CAA Gln	ACC Thr	CAA Gln	GAA Glu	AAG Lys 250	TGC Cys	CCA Pro	AAT Asn	GAG Glu	TTT Phe 255	ACT Thr	768
GGT Gly	GAT Asp	CGC Arg	TGC Cys 260	CAA Gln	AAC Asn	TAC Tyr	GTA Val	ATG Met 265	GCC Ala	AGC Ser	TTC Phe	TAC Tyr	AGT Ser 270	ACG Thr	TCC Ser	816

ACT CCC TTT CTG TCT CTG CCT GAA TAGCGCATCT CAGTCGGTGC CGCTTTCTTG	870
Thr Pro Phe Leu Ser Leu Pro Glu	
275 280	

TTGCCGCATC TCCCCTCAGA TTCCNCCTAG AGCTAGATGC GTTTTACCAG GTCTAACATT	930
GACTGCCTCT GCCTGTCGCA TGAGAACATT AACACAAGCG ATTGTATGAC TTCCTCTGTC	990
CGTGACTAGT GGGCTCTGAG CTACTCGTAG GTGCGTAAGG CTCCAGTGTT TCTGAAATTG	1050
ATCTTGAATT ACTGTGATAC GACATGATAG TCCCTCTCAC CCAGTGCAAT GACAATAAAG	1110
GCCTTGAAAA GTCAAAAAA AAAAAAAAAA	1140

(2) INFORMATION FOR SEQUENCE IDENTIFICATION NUMBER: 150:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 1764
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 150:

G AAG TCA GAA CTT CGC ATT AGC AAA GCG TCA CTG GCT GAT TCT GGA GAA	49
Lys Ser Glu Leu Arg Ile Ser Lys Ala Ser Leu Ala Asp Ser Gly Glu	
1 5 10 15	
TAT ATG TGC AAA GTG ATC AGC AAA CTA GGA AAT GAC AGT GCC TCT GCC	97
Tyr Met Cys Lys Val Ile Ser Lys Leu Gly Asn Asp Ser Ala Ser Ala	
20 25 30	
AAC ATC ACC ATT GTG GAG TCA AAC GCC ACA TCC ACA TCT ACA GCT GGG	145
Asn Ile Thr Ile Val Glu Ser Asn Ala Thr Ser Thr Ser Thr Ala Gly	
35 40 45	
ACA AGC CAT CTT GTC AAG TGT GCA GAG AAG GAG AAA ACT TTC TGT GTG	193
Thr Ser His Leu Val Lys Cys Ala Glu Lys Glu Lys Thr Phe Cys Val	
50 55 60	
AAT GGA GGC GAC TGC TTC ATG GTG AAA GAC CTT TCA AAT CCC TCA AGA	241
Asn Gly Gly Asp Cys Phe Met Val Lys Asp Leu Ser Asn Pro Ser Arg	
65 70 75 80	
TAC TTG TGC AAG TGC CAA CCT GGA TTC ACT GGA GCG AGA TGT ACT GAG	289
Tyr Leu Cys Lys Cys Gln Pro Gly Phe Thr Gly Ala Arg Cys Thr Glu	
85 90 95	
AAT GTG CCC ATG AAA GTC CAA ACC CAA GAA AAA GCG GAG GAG CTC TAC	337
Asn Val Pro Met Lys Val Gln Thr Gln Glu Lys Ala Glu Glu Leu Tyr	
100 105 110	
CAG AAG AGA GTG CTC ACC ATT ACC GGC ATT TGC ATC GCG CTG CTC GTG	385
Gln Lys Arg Val Leu Thr Ile Thr Gly Ile Cys Ile Ala Leu Leu Val	
115 120 125	

GTT Val	GGC Gly	ATC Ile	ATG Met	TGT Cys	GTG Val	GTG Val	GTC Val	TAC Tyr	TGC Cys	AAA Lys	ACC Thr	AAG Lys	AAA Lys	CAA Gln	CGG Arg	433
130						135					140					
AAA Lys	AAG Lys	CTT Leu	CAT His	GAC Asp	CGG Arg	CTT L u	CGG Arg	CAG Gln	AGC S r	CTT Leu	CGG Arg	TCT Ser	GAA Glu	AGA Arg	AAC Asn	481
145					150					155					160	
ACC Thr	ATG Met	ATG Met	AAC Asn	GTA Val	GCC Ala	AAC Asn	GGG Gly	CCC Pro	CAC His	CAC His	CCC Pro	AAT Asn	CCG Pro	CCC Pro	CCC Pro	529
				165					170					175		
GAG Glu	AAC Asn	GTG Val	CAG Gln	CTG Leu	GTG Val	AAT Asn	CAA Gln	TAC Tyr	GTA Val	TCT Ser	AAA Lys	AAT Asn	GTC Val	ATC Ile	TCT Ser	577
			180					185					190			
AGC Ser	GAG Glu	CAT His	ATT Ile	GTT Val	GAG Glu	AGA Arg	GAG Glu	GCG Ala	GAG Glu	AGC Ser	TCT Ser	TTT Phe	TCC Ser	ACC Thr	AGT Ser	625
		195					200					205				
CAC His	TAC Tyr	ACT Thr	TCG Ser	ACA Thr	GCT Ala	CAT His	CAT His	TCC Ser	ACT Thr	ACT Thr	GTC Val	ACT Thr	CAG Gln	ACT Thr	CCC Pro	673
	210					215					220					
AGT Ser	CAC His	AGC Ser	TGG Trp	AGC Ser	AAT Asn	GGA Gly	CAC His	ACT Thr	GAA Glu	AGC Ser	ATC Ile	ATT Ile	TCG Ser	GAA Glu	AGC Ser	721
225					230					235					240	
CAC His	TCT Ser	GTC Val	ATC Ile	GTG Val	ATG Met	TCA Ser	TCC Ser	GTA Val	GAA Glu	AAC Asn	AGT Ser	AGG Arg	CAC His	AGC Ser	AGC Ser	769
				245				250						255		
CCG Pro	ACT Thr	GGG Gly	GGC Gly	CCG Pro	AGA Arg	GGA Gly	CGT Arg	CTC Leu	AAT Asn	GGC Gly	TTG Leu	GGA Gly	GGC Gly	CCT Pro	CGT Arg	817
			260					265					270			
GAA Glu	TGT Cys	AAC Asn	AGC Ser	TTC Phe	CTC Leu	AGG Arg	CAT His	GCC Ala	AGA Arg	GAA Glu	ACC Thr	CCT Pro	GAC Asp	TCC Ser	TAC Tyr	865
		275					280					285				
CGA Arg	GAC Asp	TCT Ser	CCT Pro	CAT His	AGT Ser	GAA Glu	AGA Arg	CAT His	AAC Asn	CTT Leu	ATA Ile	GCT Ala	GAG Glu	CTA Leu	AGG Arg	913
	290					295					300					
AGA Arg	AAC Asn	AAG Lys	GCC Ala	CAC His	AGA Arg	TCC Ser	AAA Lys	TGC Cys	ATG Met	CAG Gln	ATC Ile	CAG Gln	CTT Leu	TCC Ser	GCA Ala	961
305					310					315					320	
ACT Thr	CAT His	CTT Leu	AGA Arg	GCT Ala	TCT Ser	TCC Ser	ATT Ile	CCC Pro	CAT His	TGG Trp	GCT Ala	TCA Ser	TTC Phe	TCT Ser	AAG Lys	1009
				325				330						335		

ACC	CCT	TGG	CCT	TTA	GGA	AGG	TAT	GTA	TCA	GCA	ATG	ACC	ACC	CCG	GCT	1057
Thr	Pro	Trp	Pro	Leu	Gly	Arg	Tyr	Val	S r	Ala	Met	Thr	Thr	Pro	Ala	
			340					345					350			
CGT	ATG	TCA	CCT	GTA	GAT	TTC	CAC	ACG	CCA	AGC	TCC	CCC	AAG	TCA	CCC	1105
Arg	Met	Ser	Pro	Val	Asp	Phe	His	Thr	Pro	Ser	Ser	Pro	Lys	Ser	Pro	
		355					360					365				
CCT	TCG	GAA	ATG	TCC	CCG	CCC	GTG	TCC	AGC	ACG	ACG	GTC	TCC	ATG	CCC	1153
Pro	Ser	Glu	Met	Ser	Pro	Pro	Val	Ser	Ser	Thr	Thr	Val	Ser	Met	Pro	
	370					375					380					
TCC	ATG	GCG	GTC	AGT	CCC	TTC	GTG	GAA	GAG	GAG	AGA	CCC	CTG	CTC	CTT	1201
Ser	Met	Ala	Val	Ser	Pro	Phe	Val	Glu	Glu	Glu	Arg	Pro	Leu	Leu	Leu	
	385				390					395					400	
GTG	ACG	CCA	CCA	CGG	CTG	CGG	GAG	AAG	TAT	GAC	CAC	CAC	GCC	CAG	CAA	1249
Val	Thr	Pro	Pro	Arg	Leu	Arg	Glu	Lys	Tyr	Asp	His	His	Ala	Gln	Gln	
				405					410					415		
TTC	AAC	TCG	TTC	CAC	TGC	AAC	CCC	GCG	CAT	GAG	AGC	AAC	AGC	CTG	CCC	1297
Phe	Asn	Ser	Phe	His	Cys	Asn	Pro	Ala	His	Glu	Ser	Asn	Ser	Leu	Pro	
			420					425					430			
CCC	AGC	CCC	TTG	AGG	ATA	GTG	GAG	GAT	GAG	GAA	TAT	GAA	ACG	ACC	CAG	1345
Pro	Ser	Pro	Leu	Arg	Ile	Val	Glu	Asp	Glu	Glu	Tyr	Glu	Thr	Thr	Gln	
		435					440					445				
GAG	TAC	GAA	CCA	GCT	CAA	GAG	CCG	GTT	AAG	AAA	CTC	ACC	AAC	AGC	AGC	1393
Glu	Tyr	Glu	Pro	Ala	Gln	Glu	Pro	Val	Lys	Lys	Leu	Thr	Asn	Ser	Ser	
	450					455					460					
CGG	CGG	GCC	AAA	AGA	ACC	AAG	CCC	AAT	GGT	CAC	ATT	GCC	CAC	AGG	TTG	1441
Arg	Arg	Ala	Lys	Arg	Thr	Lys	Pro	Asn	Gly	His	Ile	Ala	His	Arg	Leu	
	465				470					475					480	
GAA	ATG	GAC	AAC	AAC	ACA	GGC	GCT	GAC	AGC	AGT	AAC	TCA	GAG	AGC	GAA	1489
Glu	Met	Asp	Asn	Asn	Thr	Gly	Ala	Asp	Ser	Ser	Asn	Ser	Glu	Ser	Glu	
				485					490					495		
ACA	GAG	GAT	GAA	AGA	GTA	GGA	GAA	GAT	ACG	CCT	TTC	CTG	GCC	ATA	CAG	1537
Thr	Glu	Asp	Glu	Arg	Val	Gly	Glu	Asp	Thr	Pro	Phe	Leu	Ala	Ile	Gln	
			500					505					510			
AAC	CCC	CTG	GCA	GCC	AGT	CTC	GAG	GCG	GCC	CCT	GCC	TTC	CGC	CTG	GTC	1585
Asn	Pro	Leu	Ala	Ala	Ser	Leu	Glu	Ala	Ala	Pro	Ala	Phe	Arg	Leu	Val	
		515					520					525				
GAC	AGC	AGG	ACT	AAC	CCA	ACA	GGC	GGC	TTC	TCT	CCG	CAG	GAA	GAA	TTG	1633
Asp	Ser	Arg	Thr	Asn	Pro	Thr	Gly	Gly	Phe	Ser	Pro	Gln	Glu	Glu	Leu	
	530					535					540					

CAG GCC AGG CTC TCC GGT GTA ATC GCT AAC CAA GAC CCT ATC GCT GTC 1681
 Gln Ala Arg Leu Ser Gly Val Ile Ala Asn Gln Asp Pro Ile Ala Val
 545 550 555 560

TAAAACCGAA ATACACCCAT AGATTCACCT GTAAAACTTT ATTTTATATA ATAAAGTATT 1741
 CCACCTTAAA TTAAACAAAA AAA 1764

(2) INFORMATION FOR SEQUENCE IDENTIFICATION NUMBER: 151:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 50
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 151:

Lys Cys Ala Glu Lys Glu Lys Thr Phe Cys Val Asn Gly Gly Glu Cys
 1 5 10 15

Phe Met Val Lys Asp Leu Ser Asn Pro Ser Arg Tyr Leu Cys Lys Cys
 20 25 30

Pro Asn Glu Phe Thr Gly Asp Arg Cys Gln Asn Tyr Val Met Ala Ser
 35 40 45

Phe Tyr
 50

(2) INFORMATION FOR SEQUENCE IDENTIFICATION NUMBER: 152:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 50
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 152:

Lys Cys Ala Glu Lys Glu Lys Thr Phe Cys Val Asn Gly Gly Glu Cys
 1 5 10 15

Phe Met Val Lys Asp Leu Ser Asn Pro Ser Arg Tyr Leu Cys Lys Cys
 20 25 30

Gln Pro Gly Phe Thr Gly Ala Arg Cys Thr Glu Asn Val Pro Met Lys
 35 40 45

Val Gln
 50

(2) INFORMATION FOR SEQUENCE IDENTIFICATION NUMBER: 153:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 46
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 153:

Glu	Cys	Leu	Arg	Lys	Tyr	Lys	Asp	Phe	Cys	Ile	His	Gly	Glu	Cys	Lys	
1				5					10					15		
Tyr	Val	Lys	Glu	Leu	Arg	Ala	Pro	Ser	Cys	Lys	Cys	Gln	Gln	Glu	Tyr	
		20						25					30			
Phe	Gly	Glu	Arg	Cys	Gly	Glu	Lys	Ser	Asn	Lys	Thr	His	Ser			
		35					40					45				

(2) INFORMATION FOR SEQUENCE IDENTIFICATION NUMBER: 154:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 198
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 154:

AGC	CAT	CTT	GTC	AAG	TGT	GCA	GAG	AAG	GAG	AAA	ACT	TTC	TGT	GTG	AAT	48
S r	His	Leu	Val	Lys	Cys	Ala	Glu	Lys	Glu	Lys	Thr	Phe	Cys	Val	Asn	
1				5				10						15		
GGA	GGC	GAG	TGC	TTC	ATG	GTG	AAA	GAC	CTT	TCA	AAT	CCC	TCA	AGA	TAC	96
Gly	Gly	Glu	Cys	Phe	Met	Val	Lys	Asp	Leu	Ser	Asn	Pro	Ser	Arg	Tyr	
		20						25					30			
TTG	TGC	AAG	TGC	CCA	AAT	GAG	TTT	ACT	GGT	GAT	CGC	TGC	CAA	AAC	TAC	144
Leu	Cys	Lys	Cys	Pro	Asn	Glu	Phe	Thr	Gly	Asp	Arg	Cys	Gln	Asn	Tyr	
		35					40					45				
GTA	ATG	GCC	AGC	TTC	TAC	AGT	ACG	TCC	ACT	CCC	TTT	CTG	TCT	CTG	CCT	192
Val	Met	Ala	Ser	Phe	Tyr	Ser	Thr	Ser	Thr	Pro	Phe	Leu	Ser	Leu	Pro	
		50				55					60					
GAA	TAG															198
Glu																
65																

(2) INFORMATION FOR SEQUENCE IDENTIFICATION NUMBER: 155:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 192
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 155:

AGC CAT CTT GTC AAG TGT GCA GAG AAG GAG AAA ACT TTC TGT GTG AAT 48
Ser His Leu Val Lys Cys Ala Glu Lys Glu Lys Thr Phe Cys Val Asn
1 5 10 15
GGA GGC GAG TGC TTC ATG GTG AAA GAC CTT TCA AAT CCC TCA AGA TAC 96
Gly Gly Glu Cys Phe Met Val Lys Asp Leu Ser Asn Pro Ser Arg Tyr
20 25 30
TTG TGC AAG TGC CAA CCT GGA TTC ACT GGA GCG AGA TGT ACT GAG AAT 144
L u Cys Lys Cys Gln Pro Gly Phe Thr Gly Ala Arg Cys Thr Glu Asn
35 40 45
GTG CCC ATG AAA GTC CAA ACC CAA GAA AAA GCG GAG GAG CTC TAC TAA 192
Val Pro Met Lys Val Gln Thr Gln Glu Lys Ala Glu Glu Leu Tyr
50 55 60

(2) INFORMATION FOR SEQUENCE IDENTIFICATION NUMBER: 156:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 183
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 156:

AGC CAT CTT GTC AAG TGT GCA GAG AAG GAG AAA ACT TTC TGT GTG AAT 48
Ser His Leu Val Lys Cys Ala Glu Lys Glu Lys Thr Phe Cys Val Asn
1 5 10 15
GGA GGC GAG TGC TTC ATG GTG AAA GAC CTT TCA AAT CCC TCA AGA TAC 96
Gly Gly Glu Cys Phe Met Val Lys Asp Leu Ser Asn Pro Ser Arg Tyr
20 25 30
TTG TGC AAG TGC CCA AAT GAG TTT ACT GGT GAT CGC TGC CAA AAC TAC 144
Leu Cys Lys Cys Pro Asn Glu Phe Thr Gly Asp Arg Cys Gln Asn Tyr
35 40 45
GTA ATG GCC AGC TTC TAC AAA GCG GAG GAG CTC TAC TAA 183
Val Met Ala Ser Phe Tyr Lys Ala Glu Glu Leu Tyr
50 55 60

(2) INFORMATION FOR SEQUENCE IDENTIFICATION NUMBER: 157:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 210
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 157:

AGC CAT CTT GTC AAG TGT GCA GAG AAG GAG AAA ACT TTC TGT GTG AAT 48
Ser His Leu Val Lys Cys Ala Glu Lys Glu Lys Thr Phe Cys Val Asn
1 5 10 15

GGA GGC GAG TGC TTC ATG GTG AAA GAC CTT TCA AAT CCC TCA AGA TAC 96
Gly Gly Glu Cys Phe Met Val Lys Asp Leu Ser Asn Pro Ser Arg Tyr
20 25 30

TTG TGC AAG TGC CCA AAT GAG TTT ACT GGT GAT CGC TGC CAA AAC TAC 144
Leu Cys Lys Cys Pro Asn Glu Phe Thr Gly Asp Arg Cys Gln Asn Tyr
35 40 45

GTA ATG GCC AGC TTC TAC AAG CAT CTT GGG ATT GAA TTT ATG GAG AAA 192
Val Met Ala Ser Phe Tyr Lys His Leu Gly Ile Glu Phe Met Glu Lys
50 55 60

GCG GAG GAG CTC TAC TAA 210
Ala Glu Glu Leu Tyr
65

(2) INFORMATION FOR SEQUENCE IDENTIFICATION NUMBER: 158:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 267
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 158:

AGC CAT CTT GTC AAG TGT GCA GAG AAG GAG AAA ACT TTC TGT GTG AAT 48
S r His Leu Val Lys Cys Ala Glu Lys Glu Lys Thr Phe Cys Val Asn
1 5 10 15

GGA GGC GAG TGC TTC ATG GTG AAA GAC CTT TCA AAT CCC TCA AGA TAC 96
Gly Gly Glu Cys Phe Met Val Lys Asp Leu Ser Asn Pro Ser Arg Tyr
20 25 30

TTG TGC AAG TGC CAA CCT GGA TTC ACT GGA GCG AGA TGT ACT GAG AAT 144
Leu Cys Lys Cys Gln Pro Gly Phe Thr Gly Ala Arg Cys Thr Glu Asn
35 40 45

GTG	CCC	ATG	AAA	GTC	CAA	ACC	CAA	GAA	AAG	TGC	CCA	AAT	GAG	TTT	ACT	192
Val	Pro	Met	Lys	Val	Gln	Thr	Gln	Glu	Lys	Cys	Pro	Asn	Glu	Phe	Thr	
	50					55					60					
GGT	GAT	CGC	TGC	CAA	AAC	TAC	GTA	ATG	GCC	AGC	TTC	TAC	AGT	ACG	TCC	240
Gly	Asp	Arg	Cys	Gln	Asn	Tyr	Val	Met	Ala	Ser	Ph	Tyr	Ser	Thr	Ser	
65					70					75					80	
ACT	CCC	TTT	CTG	TCT	CTG	CCT	GAA	TAG								267
Thr	Pro	Phe	Leu	Ser	Leu	Pro	Glu									
				85												

(2) INFORMATION FOR SEQUENCE IDENTIFICATION NUMBER: 159:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 252
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 159:

AGC	CAT	CTT	GTC	AAG	TGT	GCA	GAG	AAG	GAG	AAA	ACT	TTC	TGT	GTG	AAT	48
Ser	His	Leu	Val	Lys	Cys	Ala	Glu	Lys	Glu	Lys	Thr	Phe	Cys	Val	Asn	
				5					10					15		
GGA	GGC	GAG	TGC	TTC	ATG	GTG	AAA	GAC	CTT	TCA	AAT	CCC	TCA	AGA	TAC	96
Gly	Gly	Glu	Cys	Phe	Met	Val	Lys	Asp	Leu	Ser	Asn	Pro	Ser	Arg	Tyr	
			20					25					30			
TTG	TGC	AAG	TGC	CAA	CCT	GGA	TTC	ACT	GGA	GCG	AGA	TGT	ACT	GAG	AAT	144
Leu	Cys	Lys	Cys	Gln	Pro	Gly	Phe	Thr	Gly	Ala	Arg	Cys	Thr	Glu	Asn	
		35					40					45				
GTG	CCC	ATG	AAA	GTC	CAA	ACC	CAA	GAA	AAG	TGC	CCA	AAT	GAG	TTT	ACT	192
Val	Pro	Met	Lys	Val	Gln	Thr	Gln	Glu	Lys	Cys	Pro	Asn	Glu	Phe	Thr	
	50					55					60					
GGT	GAT	CGC	TGC	CAA	AAC	TAC	GTA	ATG	GCC	AGC	TTC	TAC	AAA	GCG	GAG	240
Gly	Asp	Arg	Cys	Gln	Asn	Tyr	Val	Met	Ala	Ser	Phe	Tyr	Lys	Ala	Glu	
65					70					75					80	
GAG	CTC	TAC	TAA													252
Glu	Leu	Tyr														

(2) INFORMATION FOR SEQUENCE IDENTIFICATION NUMBER: 160:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 128
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: singl
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 160:

CC ACA TCC ACA TCT ACA GCT GGG ACA AGC CAT CTT GTC AAG TGT GCA 47
Thr Ser Thr Ser Thr Ala Gly Thr Ser His Leu Val Lys Cys Ala
1 5 10 15

GAG AAG GAG AAA ACT TTC TGT GTG AAT GGA GGC GAG TGC TTC ATG GTG 95
Glu Lys Glu Lys Thr Phe Cys Val Asn Gly Gly Glu Cys Phe Met Val
20 25 30

AAA GAC CTT TCA AAT CCC TCA AGA TAC TTG T GC 128
Lys Asp Leu Ser Asn Pro Ser Arg Tyr Leu
35 40

(2) INFORMATION FOR SEQUENCE IDENTIFICATION NUMBER: 161:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 141
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 161:

A CAT AAC CTT ATA GCT GAG CTA AGG AGA AAC AAG GCC CAC AGA TCC 46
His Asn Leu Ile Ala Glu Leu Arg Arg Asn Lys Ala His Arg Ser
1 5 10 15

AAA TGC ATG CAG ATC CAG CTT TCC GCA ACT CAT CTT AGA GCT TCT TCC 94
Lys Cys Met Gln Ile Gln Leu Ser Ala Thr His Leu Arg Ala Ser Ser
20 25 30

ATT CCC CAT TGG GCT TCA TTC TCT AAG ACC CCT TGG CCT TTA GGA AG 141
Ile Pro His Trp Ala Ser Phe Ser Lys Thr Pro Trp Pro Leu Gly Arg
35 40 45

- (2) INFORMATION FOR SEQUENCE IDENTIFICATION NUMBER: 162:
- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 24
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS:
 - (D) TOPOLOGY: linear
- (ix) FEATURE:
- (D) OTHER INFORMATION: Xaa in positions 15 and 22 is unknown.
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 162:

Ala Ala Glu Lys Glu Lys Thr Phe Cys Val Asn Gly Gly Glu Xaa Phe
 1 5 10 15
 Met Val Lys Asp Leu Xaa Asn Pro
 20

- (2) INFORMATION FOR SEQUENCE IDENTIFICATION NUMBER: 163:
- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 745
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 163:

00736070952207

ATG AGA TGG CGA CGC GCC CCG CGC CGC TCC GGG CGT CCC GGC CCC CGG	48
Met Arg Trp Arg Arg Ala Pro Arg Arg Ser Gly Arg Pro Gly Pro Arg	
1 5 10 15	
GCC CAG CGC CCC GGC TCC GCC GCC CGC TCG TCG CCG CCG CTG CCG CTG	96
Ala Gln Arg Pro Gly Ser Ala Ala Arg Ser Ser Pro Pro Leu Pro Leu	
20 25 30	
CTG CCA CTA CTG CTG CTG CTG GGG ACC GCG GCC CTG GCG CCG GGG GCG	144
Leu Pro Leu Leu Leu Leu Leu Gly Thr Ala Ala Leu Ala Pro Gly Ala	
35 40 45	
GCG GCC GGC AAC GAG GCG GCT CCC GCG GGG GCC TCG GTG TGC TAC TCG	192
Ala Ala Gly Asn Glu Ala Ala Pro Ala Gly Ala Ser Val Cys Tyr Ser	
50 55 60	
TCC CCG CCC AGC GTG GGA TCG GTG CAG GAG CTA GCT CAG CGC GCC GCG	240
Ser Pro Pro Ser Val Gly Ser Val Gln Glu Leu Ala Gln Arg Ala Ala	
65 70 75 80	
GTG GTG ATC GAG GGA AAG GTG CAC CCG CAG CGG CGG CAG CAG GGG GCA	288
Val Val Ile Glu Gly Lys Val His Pro Gln Arg Arg Gln Gln Gly Ala	
85 90 95	

55220T" 5T09E 230

CTC	GAC	AGG	AAG	GCG	GCG	GCG	GCG	GCG	GGC	GAG	GCA	GGG	GCG	TGG	GGC	336
Leu	Asp	Arg	Lys	Ala	Ala	Ala	Ala	Ala	Gly	Glu	Ala	Gly	Ala	Trp	Gly	
			100						105						110	
GGC	GAT	CGC	GAG	CCG	CCA	GCC	GCG	GGC	CCA	CGG	GCG	CTG	GGG	CCG	CCC	384
Gly	Asp	Arg	Glu	Pro	Pro	Ala	Ala	Gly	Pro	Arg	Ala	Leu	Gly	Pro	Pro	
			115						120						125	
GCC	GAG	GAG	CCG	CTG	CTC	GCC	GCC	AAC	GGG	ACC	GTG	CCC	TCT	TGG	CCC	432
Ala	Glu	Glu	Pro	Leu	Leu	Ala	Ala	Asn	Gly	Thr	Val	Pro	Ser	Trp	Pro	
			130						135						140	
ACC	GCC	CCG	GTG	CCC	AGC	GCC	GGC	GAG	CCC	GGG	GAG	GAG	GCG	CCC	TAT	480
Thr	Ala	Pro	Val	Pro	Ser	Ala	Gly	Glu	Pro	Gly	Glu	Glu	Ala	Pro	Tyr	
			145												160	
CTG	GTG	AAG	GTG	CAC	CAG	GTG	TGG	GCG	GTG	AAA	GCC	GGG	GGC	TTG	AAG	528
Leu	Val	Lys	Val	His	Gln	Val	Trp	Ala	Val	Lys	Ala	Gly	Gly	Leu	Lys	
															175	
AAG	GAC	TCG	CTG	CTC	ACC	GTG	CGC	CTG	GGG	ACC	TGG	GGC	CAC	CCC	GCC	576
Lys	Asp	Ser	Leu	Leu	Thr	Val	Arg	Leu	Gly	Thr	Trp	Gly	His	Pro	Ala	
															190	
TTC	CCC	TCC	TGC	GGG	AGG	CTC	AAG	GAG	GAC	AGC	AGG	TAC	ATC	TTC	TTC	624
Phe	Pro	Ser	Cys	Gly	Arg	Leu	Lys	Glu	Asp	Ser	Arg	Tyr	Ile	Phe	Phe	
ATG	GAG	CCC	GAC	GCC	AAC	AGC	ACC	AGC	CGC	GCG	CCG	GCC	GCC	TTC	CGA	672
Met	Glu	Pro	Asp	Ala	Asn	Ser	Thr	Ser	Arg	Ala	Pro	Ala	Ala	Phe	Arg	
GCC	TCT	TTC	CCC	CCT	CTG	GAG	ACG	GGC	CGG	AAC	CTC	AAG	AAG	GAG	GTC	720
Ala	Ser	Phe	Pro	Pro	Leu	Glu	Thr	Gly	Arg	Asn	Leu	Lys	Lys	Glu	Val	
AGC	CGG	GTG	CTG	TGC	AAG	CGG	TGC	G								745
Ser	Arg	Val	Leu	Cys	Lys	Arg	Cys									

- (2) INFORMATION FOR SEQUENCE IDENTIFICATION NUMBER: 164:
- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 12
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS:
 - (D) TOPOLOGY: linear
 - (ix) FEATURE:
 - (D) OTHER INFORMATION: Xaa in position 1 is unknown.
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 164:

Xaa Ala Leu Ala Ala Ala Gly Tyr Asp Val Glu Lys
1 5 10

- (2) INFORMATION FOR SEQUENCE IDENTIFICATION NUMBER: 165:
- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 5
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS:
 - (D) TOPOLOGY: linear
 - (ix) FEATURE:
 - (D) OTHER INFORMATION: Xaa in position 1 is unknown.
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 165:

Xaa Leu Val Leu Arg
1 5

- (2) INFORMATION FOR SEQUENCE IDENTIFICATION NUMBER: 166:
- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 11
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS:
 - (D) TOPOLOGY: linear
 - (ix) FEATURE:
 - (D) OTHER INFORMATION: Xaa in positions 1, 2, and 3 is unknown.
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 166:

Xaa Xaa Xaa Tyr Pro Gly Gln Ile Thr Ser Asn
1 5 10

(2) INFORMATION FOR SEQUENCE IDENTIFICATION NUMBER: 167:
 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 60
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear
 (ix) FEATURE:
 (D) OTHER INFORMATION: N in positions 25 and 36 is unknown.

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 167:

ATAGGGAAGG GCGGGGGAAG GGTCNCCCTC NGCAGGGCCG GGCTTGCCTC TGGAGCCTCT

60

(2) INFORMATION FOR SEQUENCE IDENTIFICATION NUMBER: 168:
 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 18
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear
 (ix) FEATURE:
 (D) OTHER INFORMATION: N in position 16 is unknown.
 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 168:

TTTACACATA TATTCNCC 18

(2) INFORMATION FOR SEQUENCE IDENTIFICATION NUMBER: 169:
 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 21
 (B) TYPE: amino acid
 (C) STRANDEDNESS:
 (D) TOPOLOGY: linear
 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 169:

Glu Thr Gln Pro Asp Pro Gly Gln Ile Leu Lys Lys Val Pro Met Val
 1 5 10 15
 Ile Gly Ala Tyr Thr
 20

(2) INFORMATION FOR SEQUENCE IDENTIFICATION NUMBER: 170:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 422
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 170:

Met Arg Trp Arg Arg Ala Pro Arg Arg Ser Gly Arg Pro Gly Pro Arg
1 5 10 15
Ala Gln Arg Pro Gly Ser Ala Ala Arg Ser Ser Pro Pro Leu Pro Leu
20 25 30
Leu Pro Leu Leu Leu Leu Gly Thr Ala Ala Leu Ala Pro Gly Ala
35 40 45
Ala Ala Gly Asn Glu Ala Ala Pro Ala Gly Ala Ser Val Cys Tyr Ser
50 55 60
Ser Pro Pro Ser Val Gly Ser Val Gln Glu Leu Ala Gln Arg Ala Ala
65 70 75 80
Val Val Ile Glu Gly Lys Val His Pro Gln Arg Arg Gln Gln Gly Ala
85 90 95
Leu Asp Arg Lys Ala Ala Ala Ala Gly Glu Ala Gly Ala Trp Gly
100 105 110
Gly Asp Arg Glu Pro Pro Ala Ala Gly Pro Arg Ala Leu Gly Pro Pro
115 120 125
Ala Glu Glu Pro Leu Leu Ala Ala Asn Gly Thr Val Pro Ser Trp Pro
130 135 140
Thr Ala Pro Val Pro Ser Ala Gly Glu Pro Gly Glu Glu Ala Pro Tyr
145 150 155 160
Leu Val Lys Val His Gln Val Trp Ala Val Lys Ala Gly Gly Leu Lys
165 170 175
Lys Asp Ser Leu Leu Thr Val Arg Leu Gly Thr Trp Gly His Pro Ala
180 185 190
Phe Pro Ser Cys Gly Arg Leu Lys Glu Asp Ser Arg Tyr Ile Phe Phe
195 200 205
Met Glu Pro Asp Ala Asn Ser Thr Ser Arg Ala Pro Ala Ala Phe Arg
210 215 220

Ala Ser Phe Pro Pro Leu Glu Thr Gly Arg Asn Leu Lys Lys Glu Val
 225 230 235 240

Ser Arg Val Leu Cys Lys Arg Cys Ala Leu Pro Pro Gln Leu Lys Glu
 245 250 255

Met Lys Ser Gln Glu Ser Ala Ala Gly Ser Lys Leu Val Leu Arg Cys
 260 265 270

Glu Thr Ser Ser Glu Tyr Ser Ser Leu Arg Phe Lys Trp Phe Lys Asn
 275 280 285

Gly Asn Glu Leu Asn Arg Lys Asn Lys Pro Gln Asn Ile Lys Ile Gln
 290 295 300

Lys Lys Pro Gly Lys Ser Glu Leu Arg Ile Asn Lys Ala Ser Leu Ala
 305 310 315 320

Asp Ser Gly Glu Tyr Met Cys Lys Val Ile Ser Lys Leu Gly Asn Asp
 325 330 335

Ser Ala Ser Ala Asn Ile Thr Ile Val Glu Ser Asn Ala Thr Ser Thr
 340 345 350

S r Thr Thr Gly Thr Ser His Leu Val Lys Cys Ala Glu Lys Glu Lys
 355 360 365

Thr Phe Cys Val Asn Gly Gly Glu Cys Phe Met Val Lys Asp Leu Ser
 370 375 380

Asn Pro Ser Arg Tyr Leu Cys Lys Cys Pro Asn Glu Phe Thr Gly Asp
 385 390 395 400

Arg Cys Gln Asn Tyr Val Met Ala Ser Phe Tyr Ser Thr Ser Thr Pro
 405 410 415

Phe Leu Ser Leu Pro Glu
 420

(2) INFORMATION FOR SEQUENCE IDENTIFICATION NUMBER: 171:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 69
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 171:

Met Ser Glu Arg Lys Glu Gly Arg Gly Lys Gly Lys Gly Lys Lys Lys
 1 5 10 15

Glu Arg Gly Ser Gly Lys Lys Pro Glu Ser Ala Ala Gly Ser Gln Ser
 20 25 30
 Pro Arg Glu Ile Ile Thr Gly Met Pro Ala Ser Thr Glu Gly Ala Tyr
 35 40 45
 Val Ser Ser Glu Ser Pro Ile Arg Ile Ser Val Ser Thr Glu Gly Ala
 50 55 60
 Asn Thr Ser Ser Ser
 65

(2) INFORMATION FOR SEQUENCE IDENTIFICATION NUMBER: 172:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 19
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 172:

Arg Lys Gly Asp Val Pro Gly Pro Arg Val Lys Ser Ser Arg Ser Thr
 1 5 10 15
 Thr Thr Ala

(2) INFORMATION FOR SEQUENCE IDENTIFICATION NUMBER: 173:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 231
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 173:

CGCGAGCGCC	TCAGCGCGGC	CGCTCGCTCT	CCCCCTCGAG	GGACAAACTT	TTCCCAAACC	60
CGATCCGAGC	CCTTGGACCA	AACTCGCCTG	CGCCGAGAGC	CGTCCGCGTA	GAGCGCTCCG	120
TCTCCGGCGA	GATGTCCGAG	CGCAAAGAAG	GCAGAGGCAA	AGGGAAGGGC	AAGAAGAAGG	180
AGCGAGGCTC	CGGCAAGAAG	CCGGAGTCCG	CGGCGGGCAG	CCAGAGCCCA	G	231

(2) INFORMATION FOR SEQUENCE IDENTIFICATION NUMBER: 174:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 178
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 174:

CCTGCTCTCC	CCGATTGAAA	GAGATGAAAA	GCCAGGAATC	GGCTGCAGGT	TCCAAACTAG	60
TCCTTCGGTG	TGAAACCAGT	TCTGAATACT	CCTCTCTCAG	ATTCAAGTGG	TTCAAGAATG	120
GGAATGAATT	GAATCGAAAA	AACAAACCAC	AAAATATCAA	GATACAAAAA	AAGCCAGG	178

(2) INFORMATION FOR SEQUENCE IDENTIFICATION NUMBER: 175:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 122
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 175:

GAAGTCAGAA	CTTCGCATTA	ACAAAGCATC	ACTGGCTGAT	TCTGGAGAGT	ATATGTGCAA	60
AGTGATCAGC	AAATTAGGAA	ATGACAGTGC	CTCTGCCAAT	ATCACCATCG	TGGAATCAAA	120
CG						122

(2) INFORMATION FOR SEQUENCE IDENTIFICATION NUMBER: 176:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 102
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 176:

AGATCATCAC	TGGTATGCCA	GCCTCAACTG	AAGGAGCATA	TGTGTCTTCA	GAGTCTCCCA	60
TTAGAATATC	AGTATCCACA	GAAGGAGCAA	ATACTTCTTC	AT		102

(2) INFORMATION FOR SEQUENCE IDENTIFICATION NUMBER: 177:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 128
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 177:

CTACATCTAC ATCCACCACT GGGACAAGCC ATCTTGTAAG ATGTGCGGAG AAGGAGAAAA
CTTTCTGTGT GAATGGAGGG GAGTGCTTCA TGGTGAAAGA CCTTTCAAAC CCCTCGAGAT
ACTTGTGC

60
120
128

(2) INFORMATION FOR SEQUENCE IDENTIFICATION NUMBER: 178:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 69
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 178:

AAAGTGCCAAC CTGGATTCAC TGGAGCAAGA TGTACTGAGA ATGTGCCCAT GAAAGTCCAA
AACCAAGAA

60
69

(2) INFORMATION FOR SEQUENCE IDENTIFICATION NUMBER: 179:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 23
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 179:

TCGGGCTCCA TGAAGAAGAT GTA

23

(2) INFORMATION FOR SEQUENCE IDENTIFICATION NUMBER: 180

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 23
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 180:

TCCATGAAGA AGATGTACCT GCT

23

(2) INFORMATION FOR SEQUENCE IDENTIFICATION NUMBER: 181

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 22
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 181:

ATGTACCTGC TGTCCCTCCTT GA

22

(2) INFORMATION FOR SEQUENCE IDENTIFICATION NUMBER: 182

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 22
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 182:

TTGAAGAAGG ACTCGCTGCT CA

22

(2) INFORMATION FOR SEQUENCE IDENTIFICATION NUMBER: 183

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 20
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 183:

AAAGCCGGGG GCTTGAAGAA

20

(2) INFORMATION FOR SEQUENCE IDENTIFICATION NUMBER: 184

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 20
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 184:

ATGARGTGTG GCGGCGGAAA

20